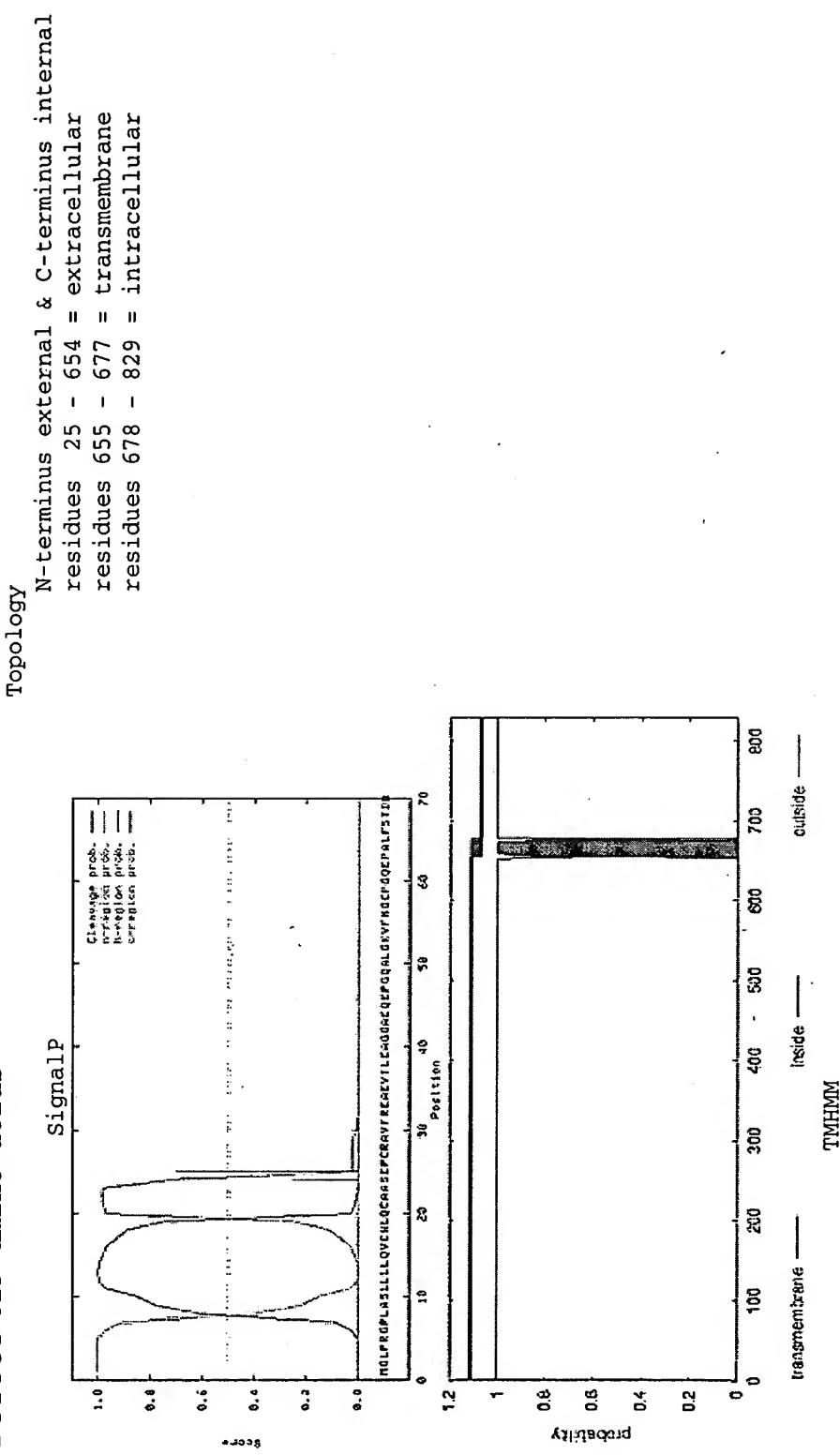


Figure 1

PCTUC5 829 amino acids

ANALYSIS
Cleaved signal peptide
Cleavage site = between position 24 and 25
MGLPRGPIASUULLQVCMWLQCAAS ↴ EPCRAVFREA...



RESULTS
signal peptide probability > 99.9%
maximum cleavage site probability = 70.2%
number of probable transmembrane regions = 1

Figure 2

RESULTS
signal peptide probability = 98.3%
maximum cleavage site probability = 41.9%
number of probable transmembrane regions = 0

PCTUC93

345 amino acids

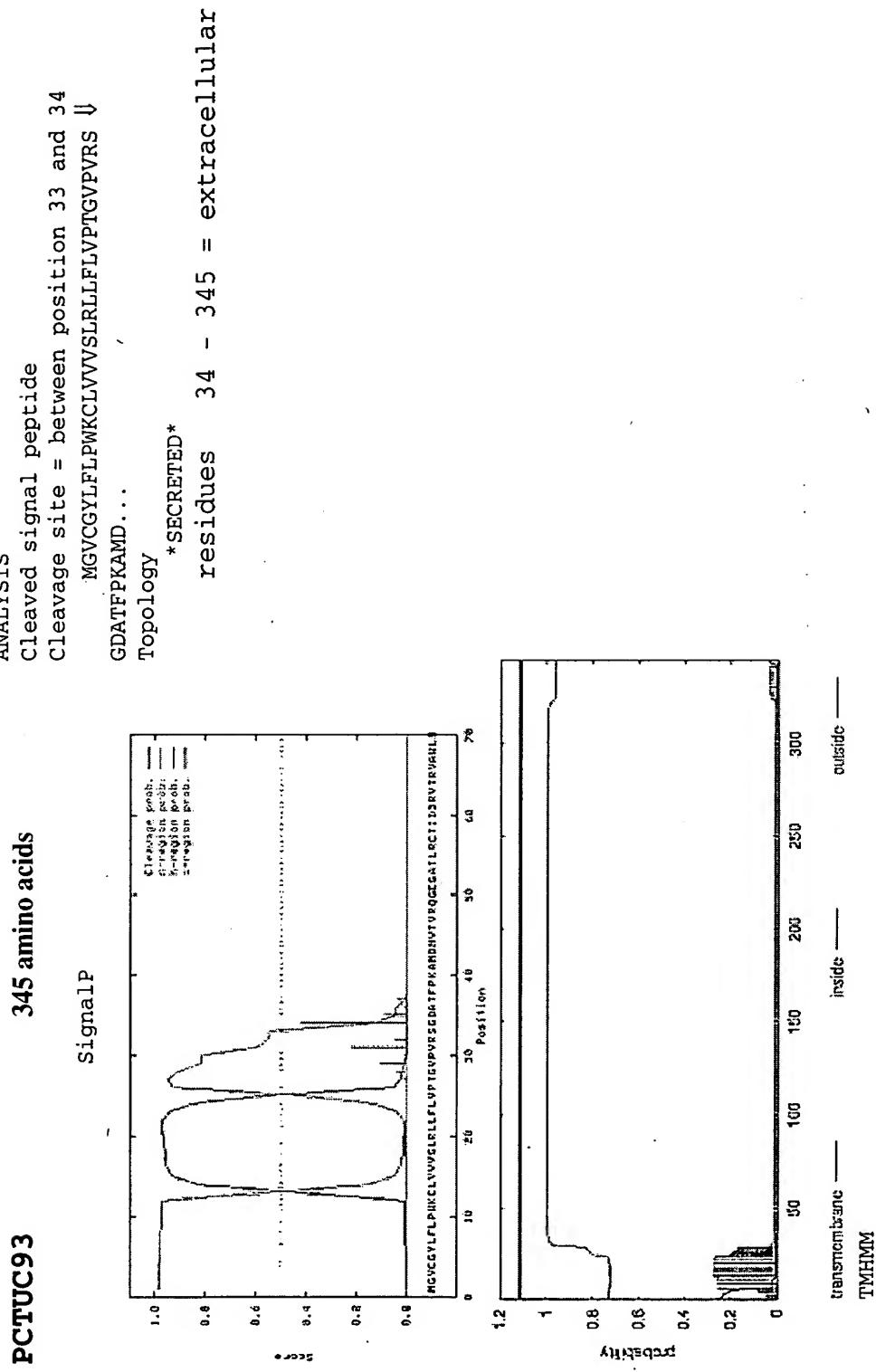
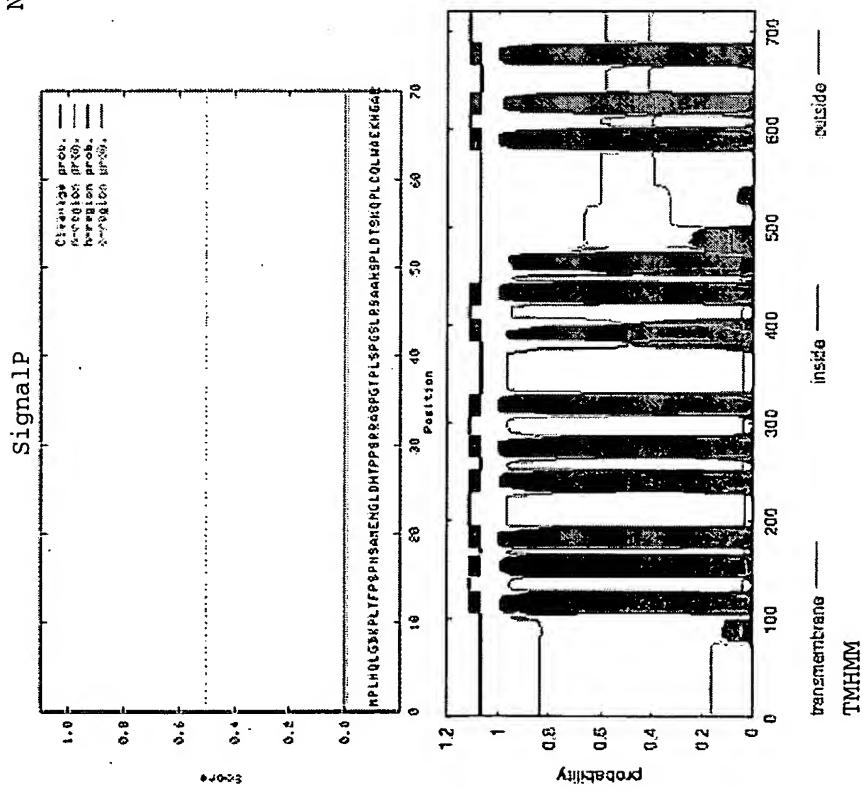


Figure 3

**ANALYSIS
N-terminal signal sequence independent membrane
insertion
Topology**



RESULTS
 signal peptide probability = 0%
 signal anchor probability = 0%
 number of probable transmembrane regions = 11

Figure 4

ANALYSIS

PCTUC239 702 amino acids

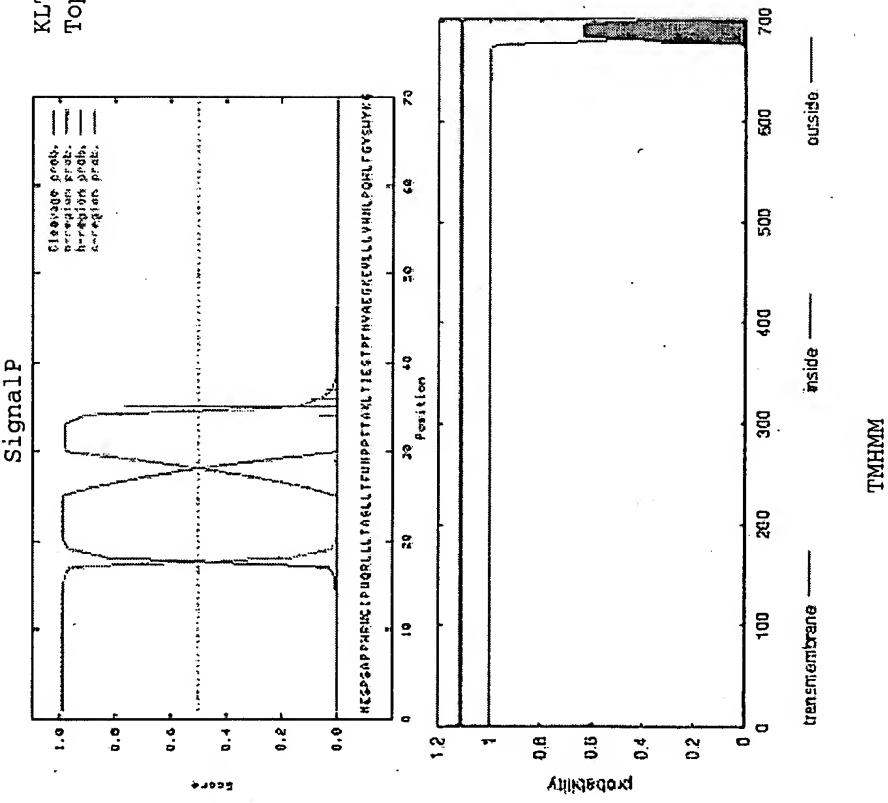
Cleaved signal peptide

Cleavage site = between position 34 and 35
MESPSAPPHRWCIPWQRLLTASLLTFWNPPPTA \Downarrow

KLTIESTPFN...

SECRETED

residues 35 - 702 = extracellular
Topology



RESULTS
signal peptide probability = 99.3%
maximum cleavage site probability = 76.5%
number of probable transmembrane regions = 0

Figure 5

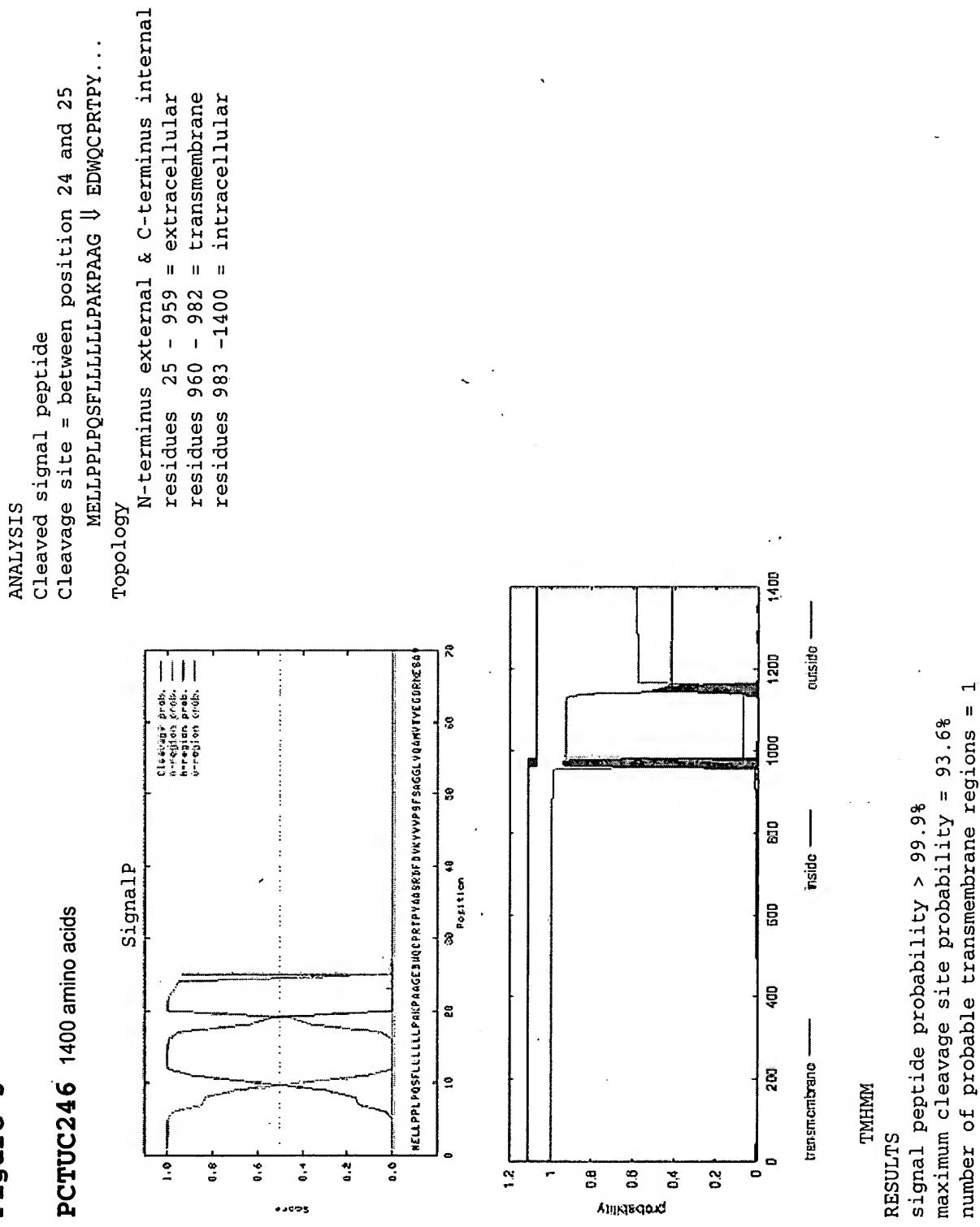


Figure 6

PCTUC360 339 amino acids
SignalP

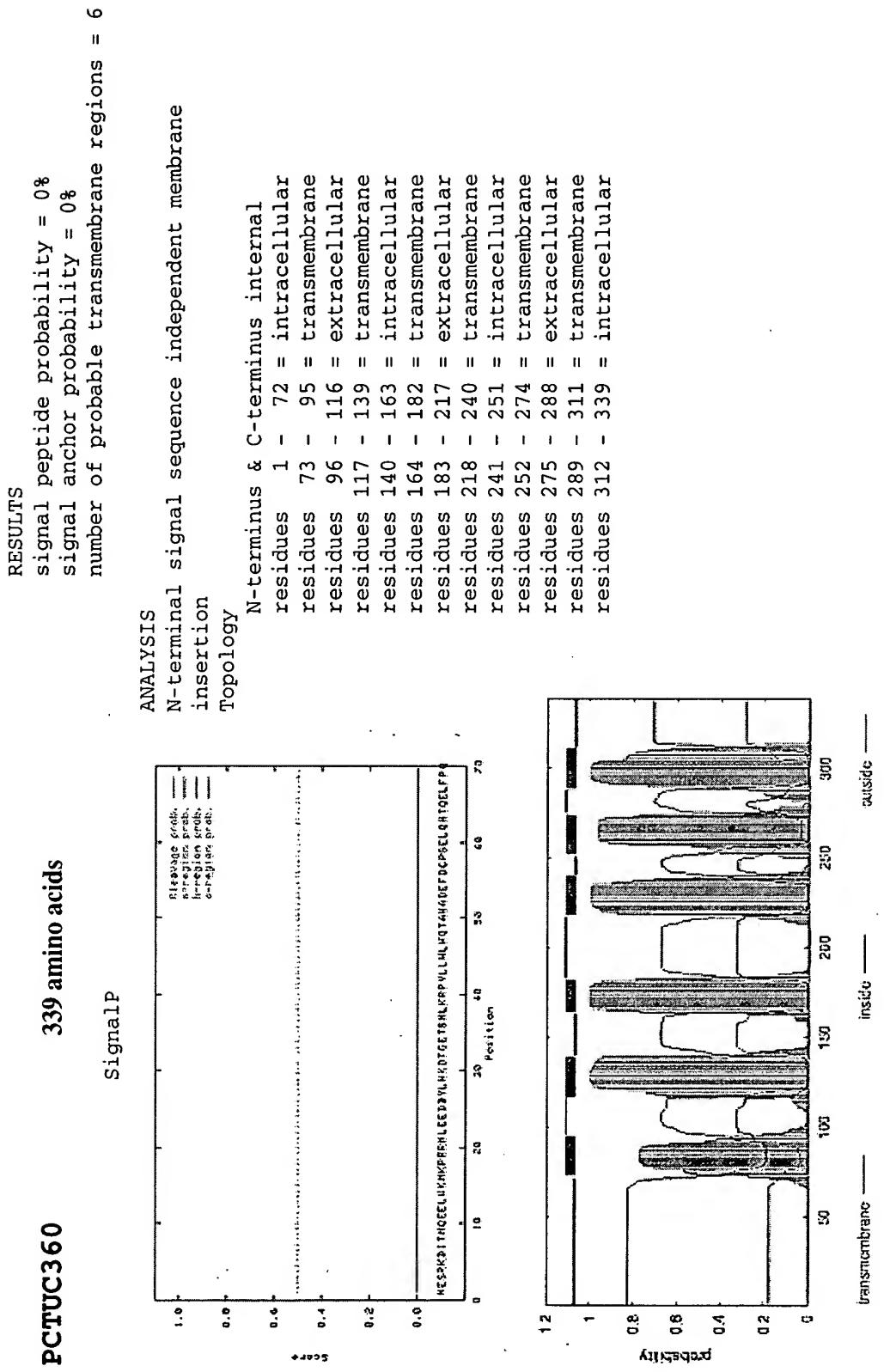
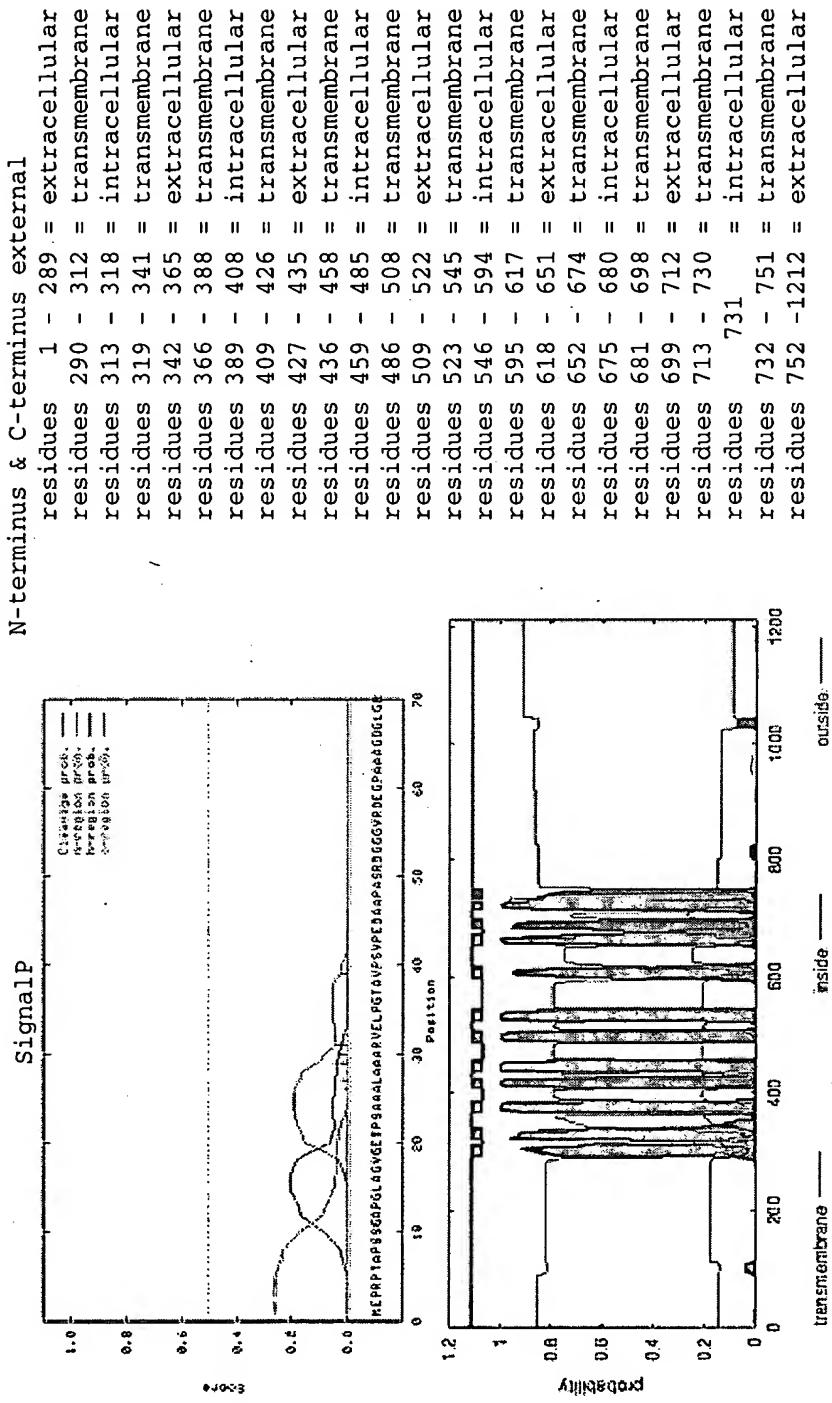


Figure 7

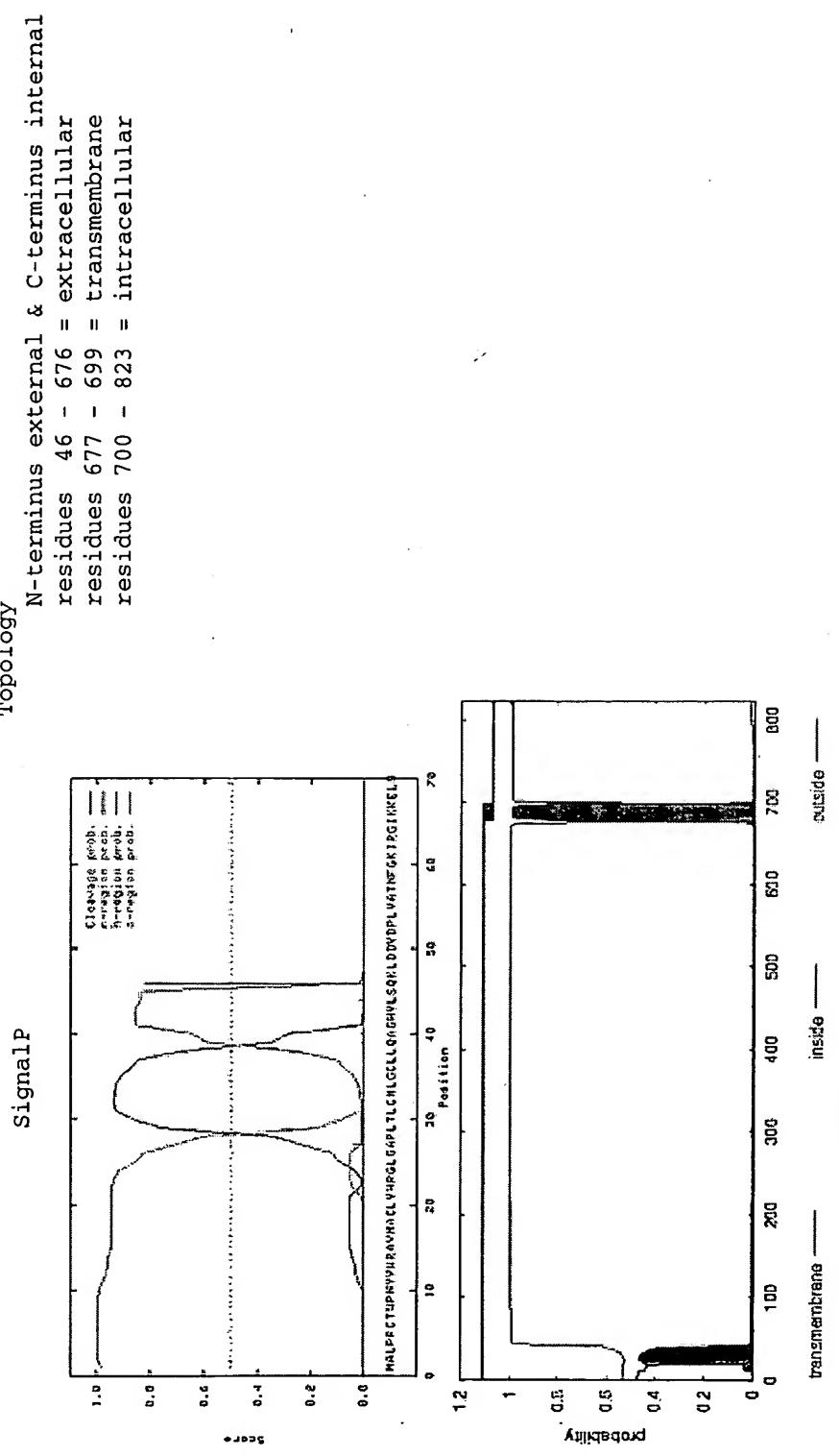
PCTUC4 62 1212 amino acids
ANALYSIS N-terminal signal sequence independent membrane insertion



RESULTS signal peptide probability = 25.9%
 signal anchor probability = 0%
 number of probable transmembrane regions = 12

Figure 8

ANALYSIS
Cleaved signal peptide
Cleavage site = between position 45 and 46
MALPRCTWENYYWRRAVMACLVHRCGLGAPLTLCMLGCLLQAGHVLS
QKLDDVDPDV...
PCTUC468 823 amino acids



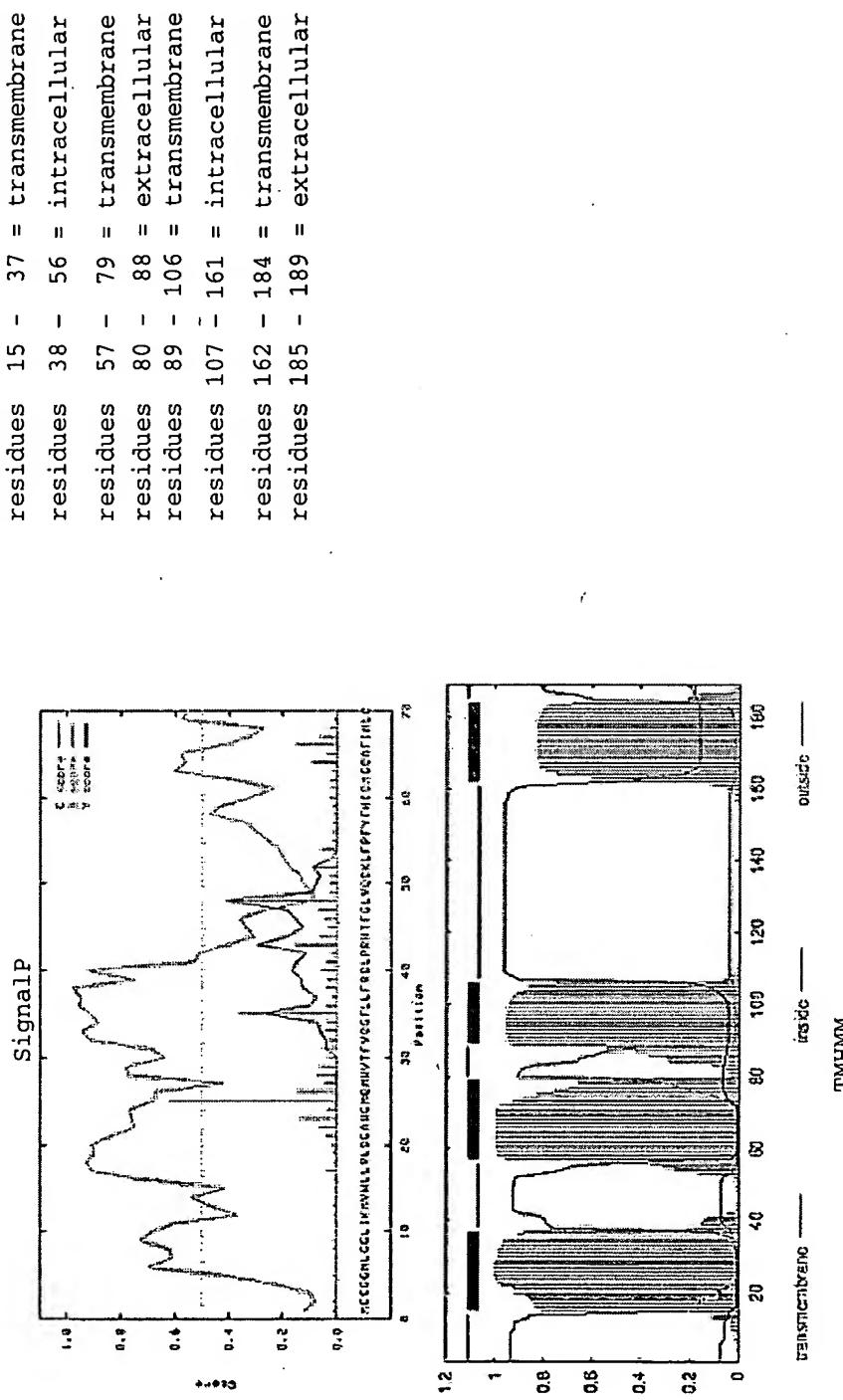
RESULTS

signal peptide probability = 98.4%
maximum cleavage site probability = 82.2%
number of probable transmembrane regions = 1

Figure 9

ANALYSIS
Signal Anchor (non-cleaved signal peptide)
Topology

PCTUC536 189 amino acids



RESULTS

signal peptide probability = 29.2%
signal anchor probability = 37.2%
number of probable transmembrane regions = 4

Figure 10

PCTUC582 349 amino acids

ANALYSIS
Cleaved signal peptide
Cleavage site = between position 34 and 35
MGPISAPSCRWRIPWQGLLLTASLUFFWNNPPTTA
QLTIEAVPSN...
Topology

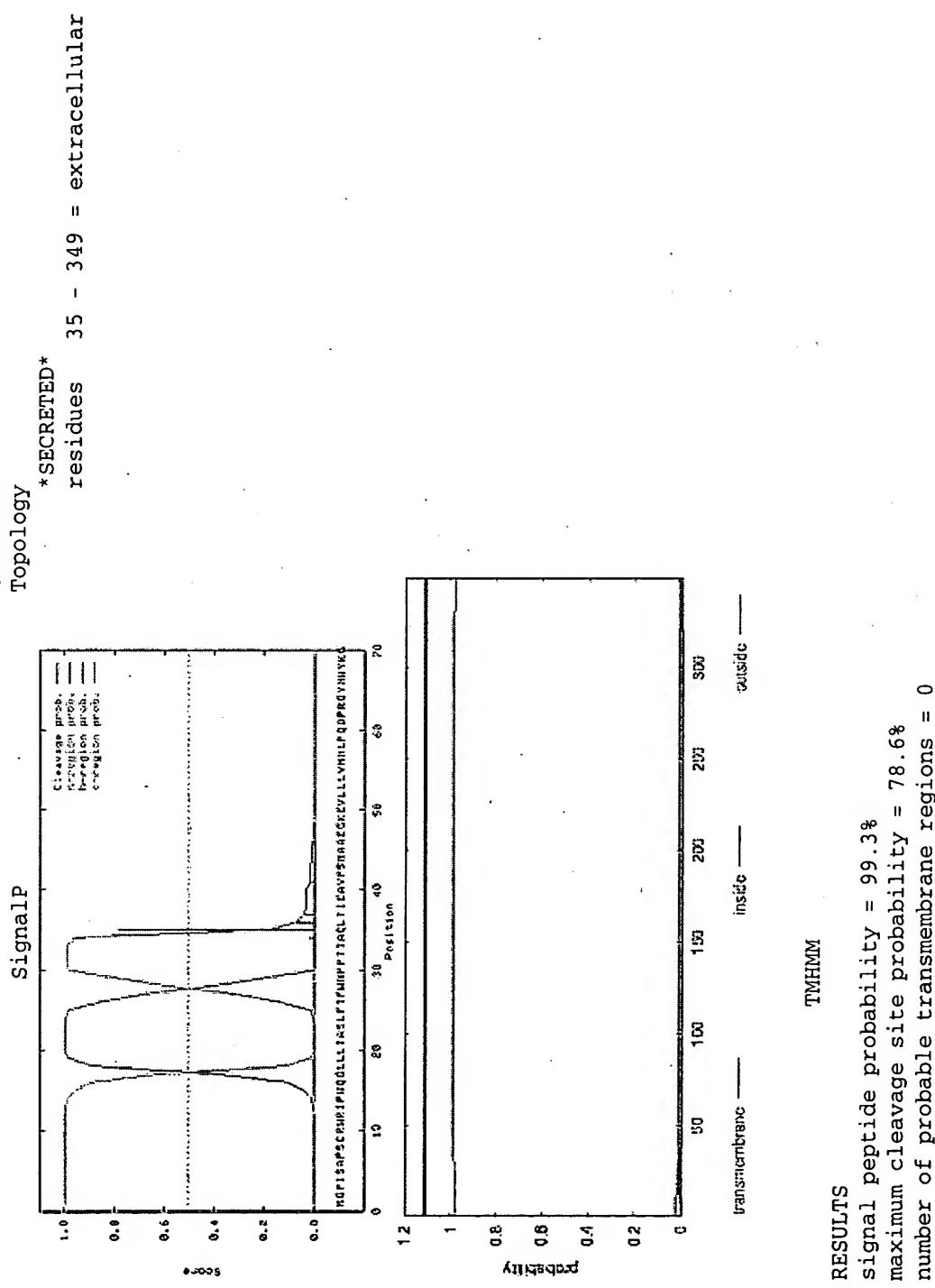
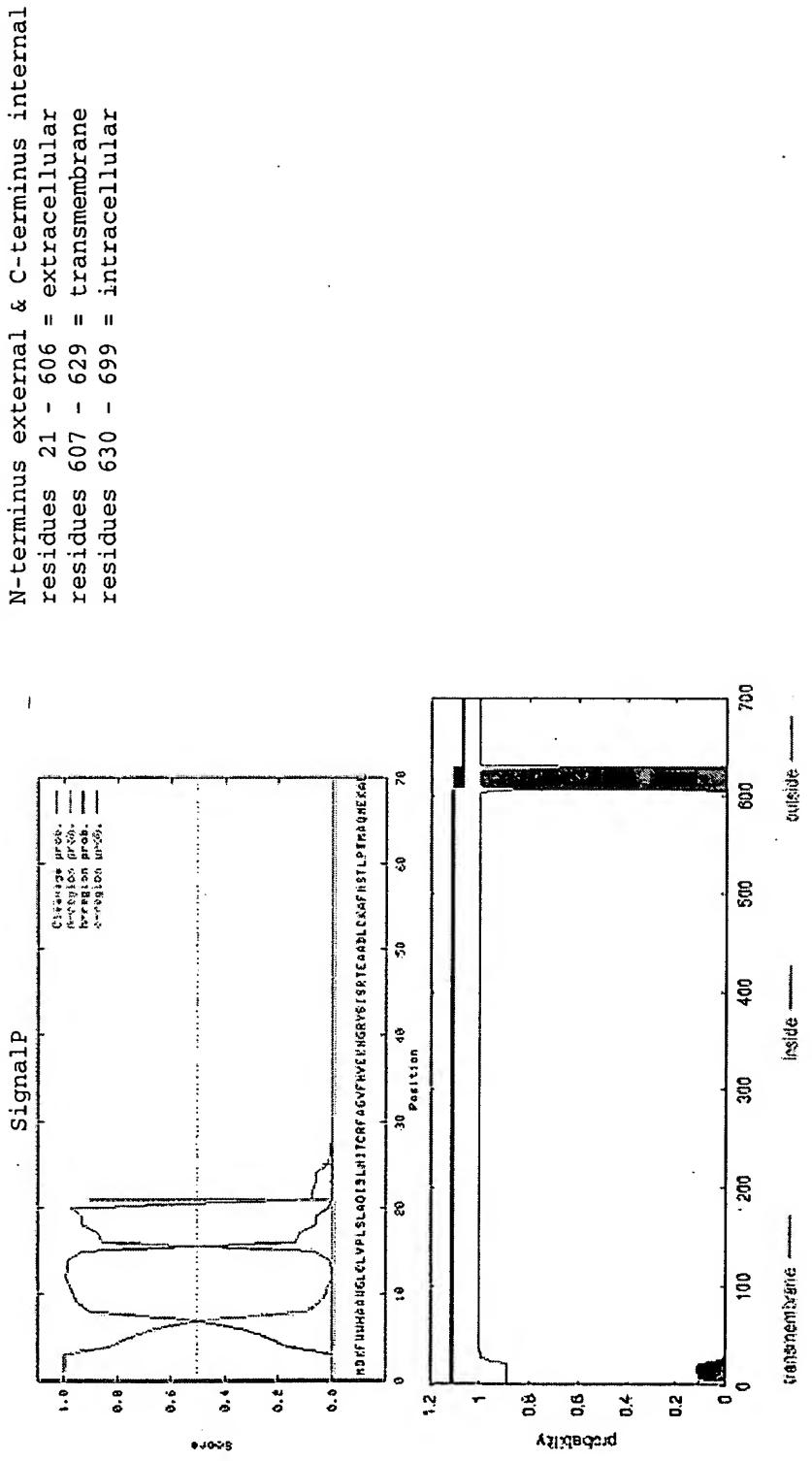


Figure 11

ANALYSIS
Cleaved signal peptide
Cleavage site = between position 20 and 21
PCTUC605 699 amino acids
MDKFWMFAAMGLCLVPLSLA ↓ QIDLNITCRF...
Topology



RESULTS
signal peptide probability = 99.7%
maximum cleavage site probability = 90.9%
number of probable transmembrane regions = 1

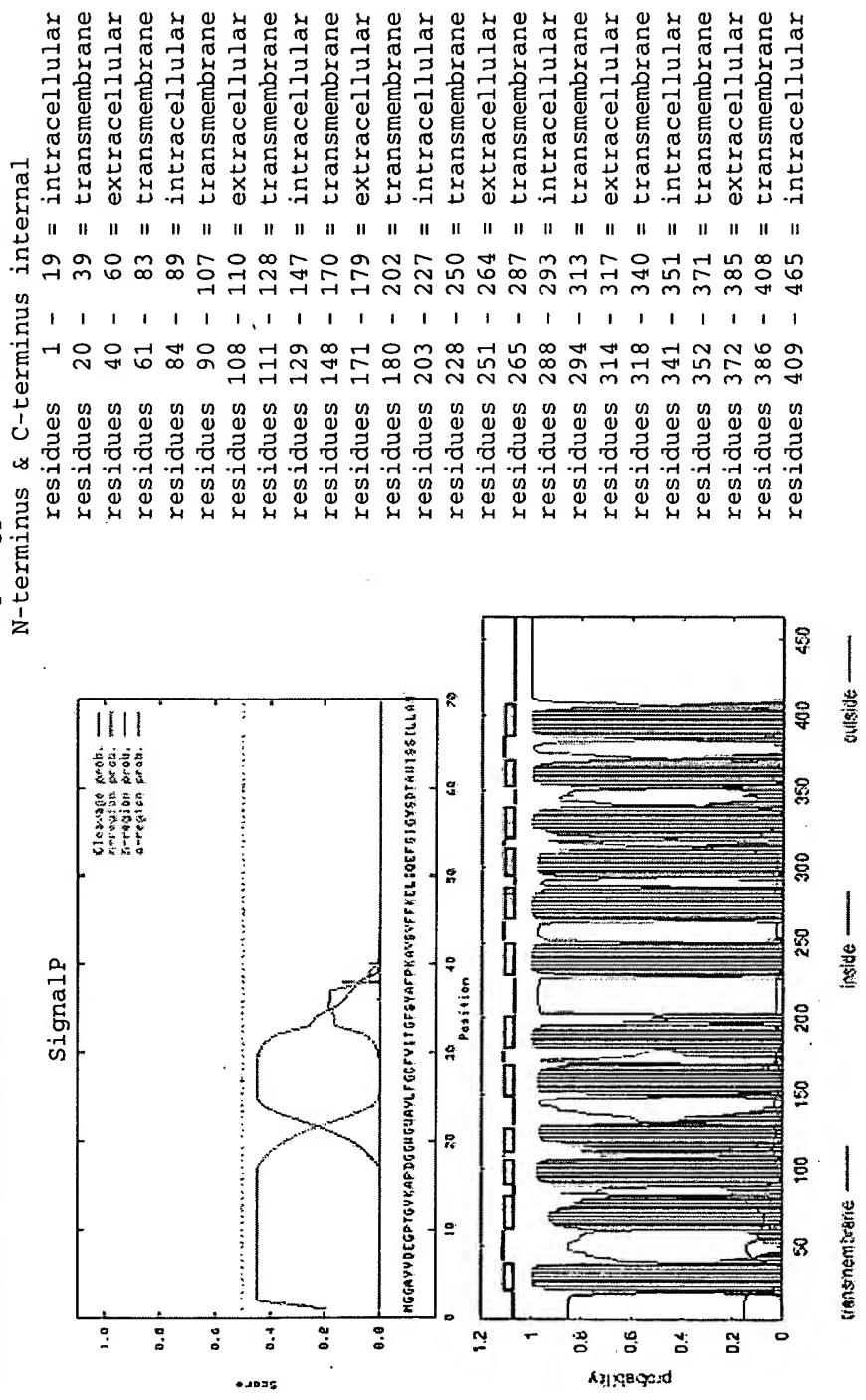
TMHMM

Figure 12

ANALYSIS
N-terminal signal sequence independent membrane
insertion

PCTUC629 465 amino acids

Topology



RESULTS

signal peptide probability = 19.3%
signal anchor probability = 25.6%
number of probable transmembrane regions = 12

12

Figure 13

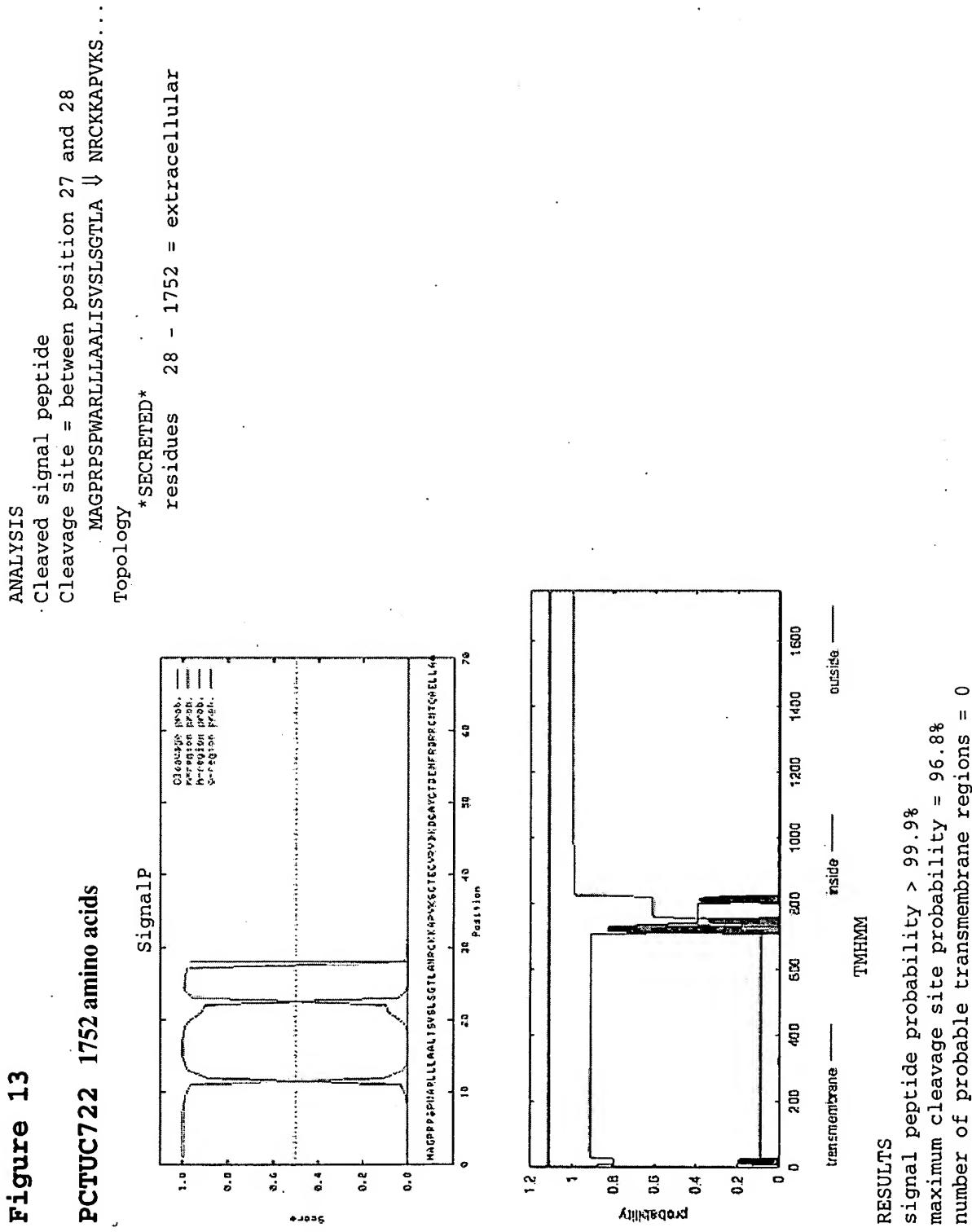


Figure 14

ANALYSIS
Signal Anchor (non-cleaved signal peptide)
Topology

PCTUC748 245 amino acids

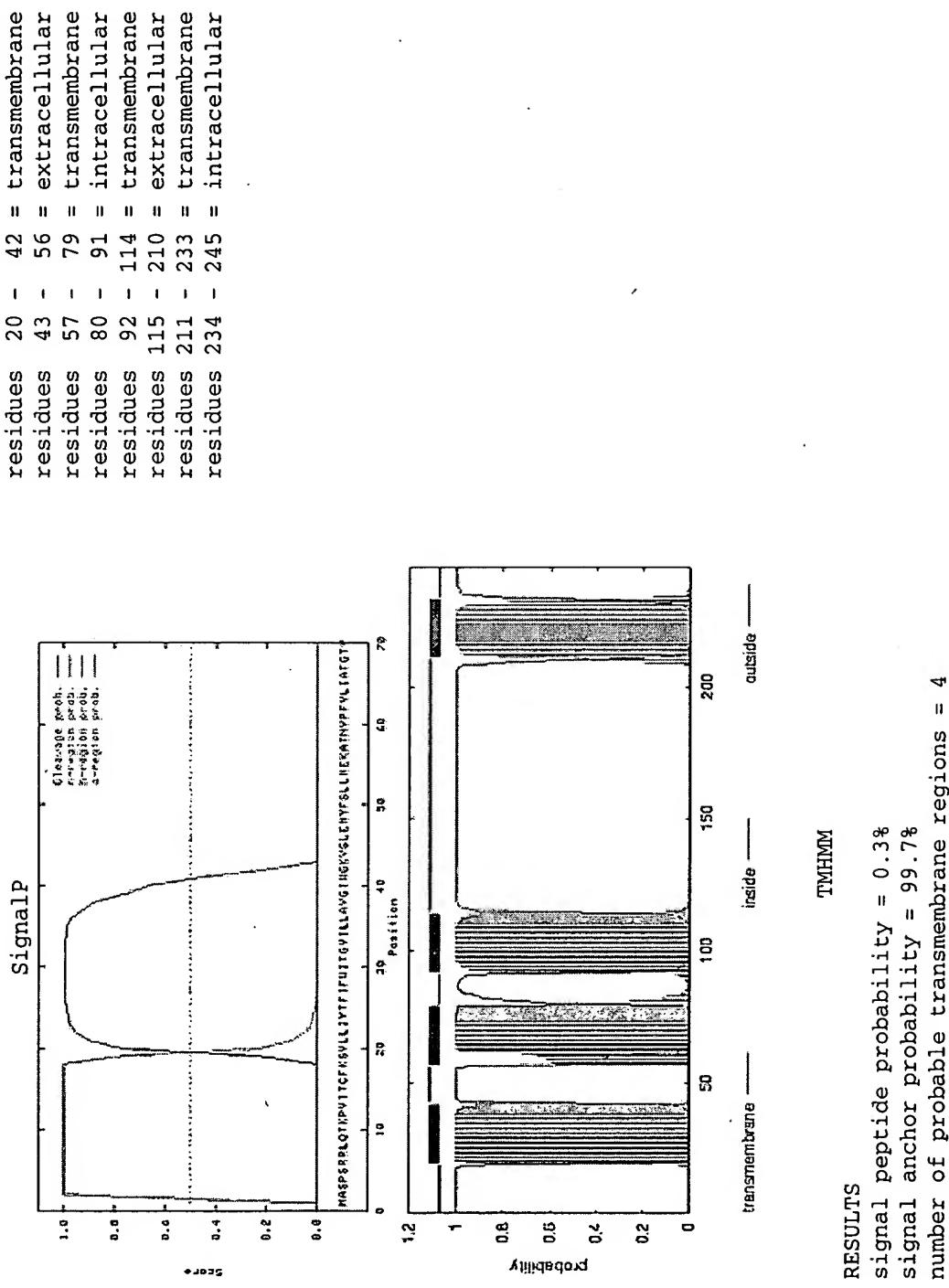
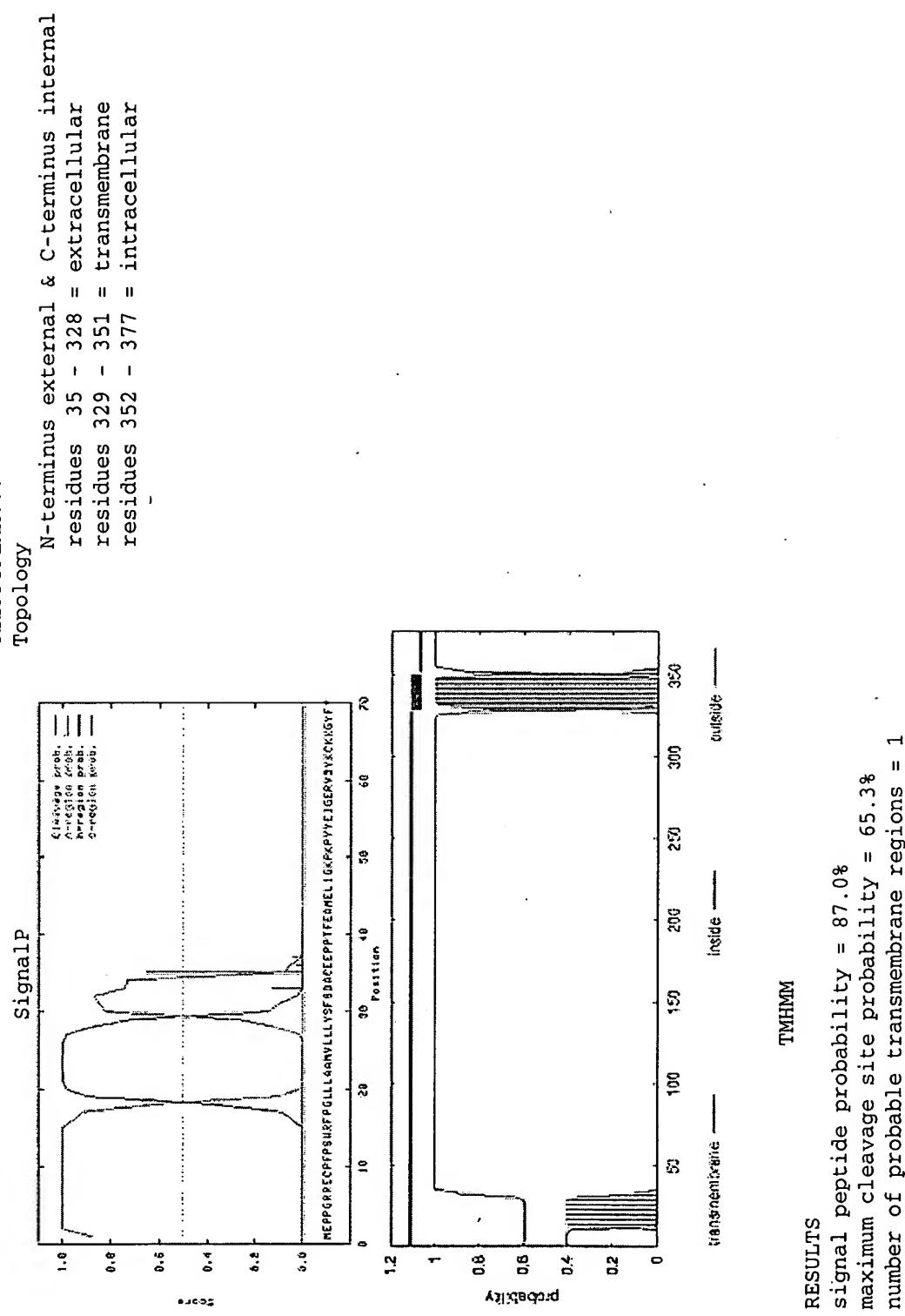


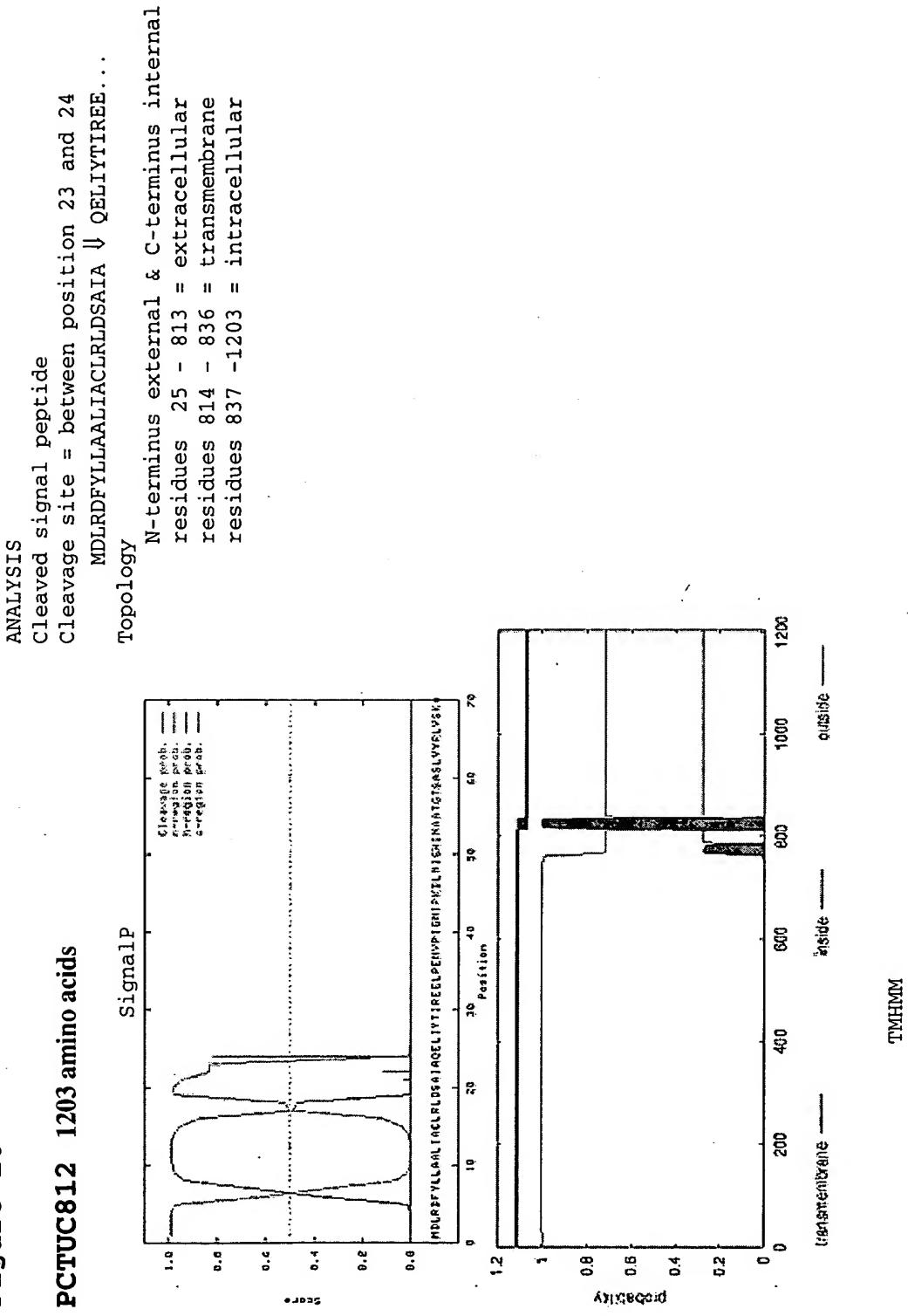
Figure 15

ANALYSIS
Cleaved signal peptide
Cleavage site = between position 34 and 35
PCTUC784 377 amino acids
MEPPGRRRECFFPSWRFPGLLLAAAMVLLLYSFSDA ↓
CEEPPPTFEAM...



RESULTS
signal peptide probability = 87.0%
maximum cleavage site probability = 65.3%
number of probable transmembrane regions = 1

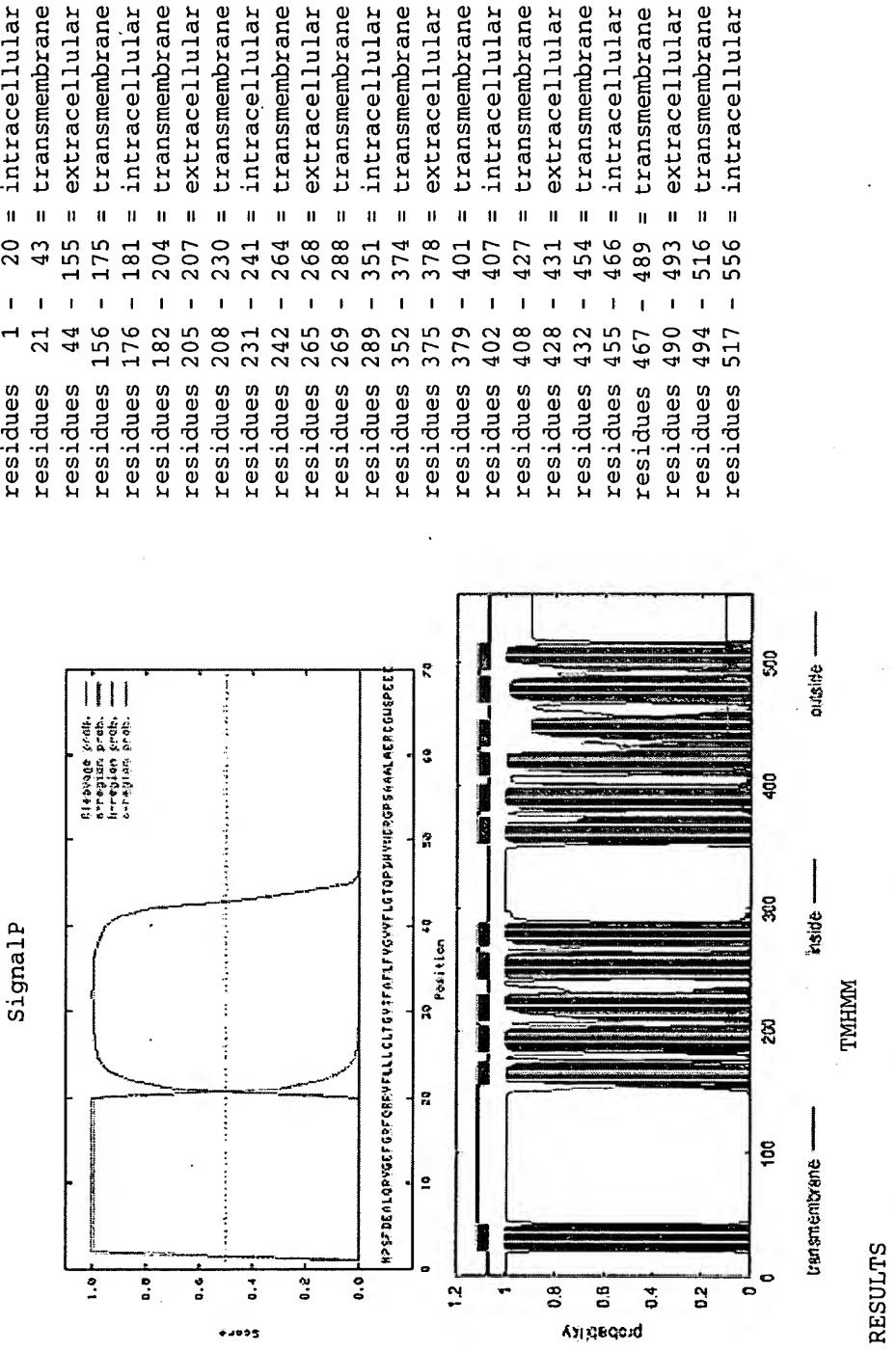
Figure 16



RESULTS
 signal peptide probability = 99.1%
 maximum cleavage site probability = 82.5%
 number of probable transmembrane regions = 1

Figure 17

ANALYSIS
Signal Anchor (non-cleaved signal peptide)
Topology
PCTUC856 556 amino acids



RESULTS
 signal peptide probability = 0.18
 signal anchor probability = 99.9%
 number of probable transmembrane regions = 12

Figure 18
PCTUC898 807 amino acids

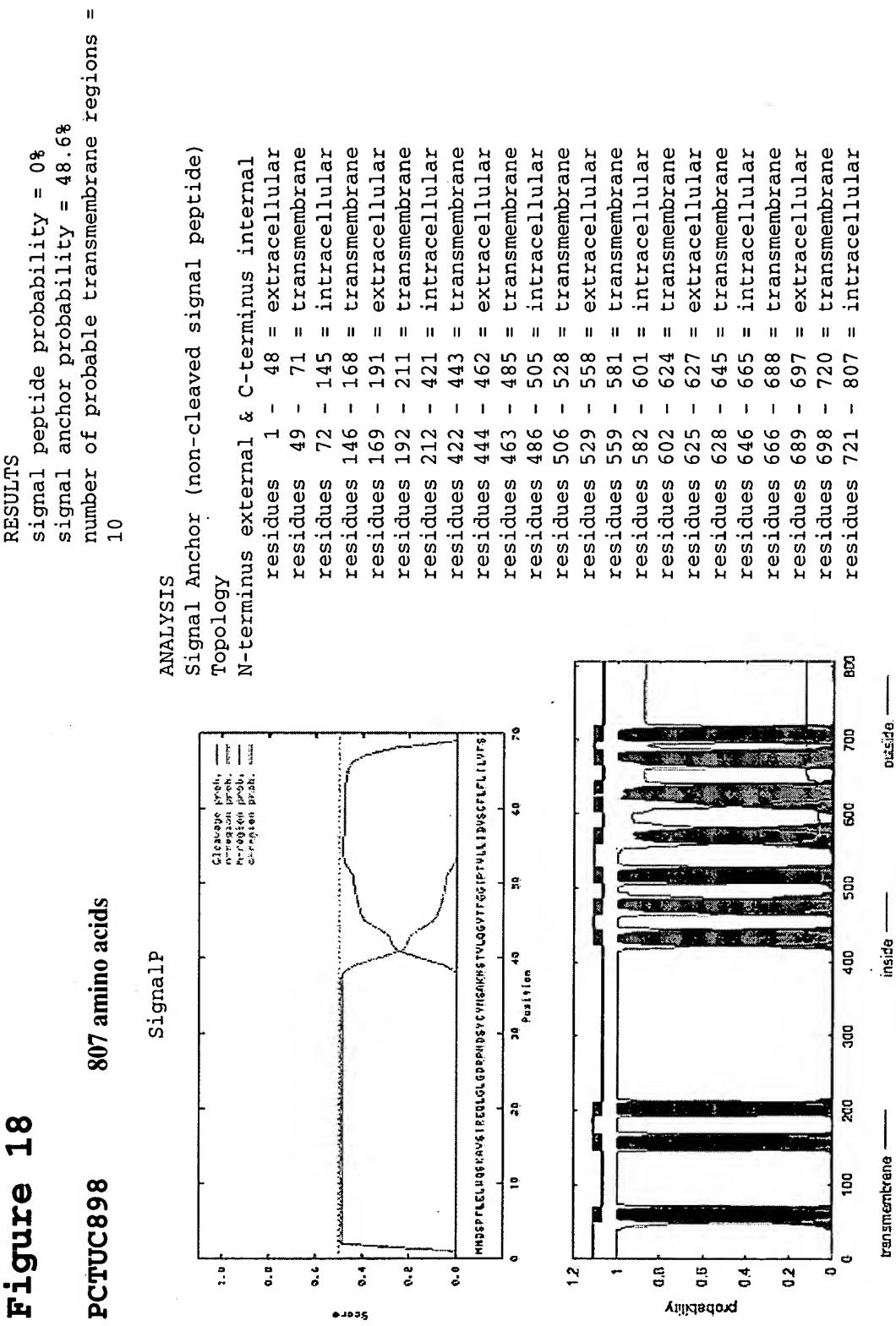
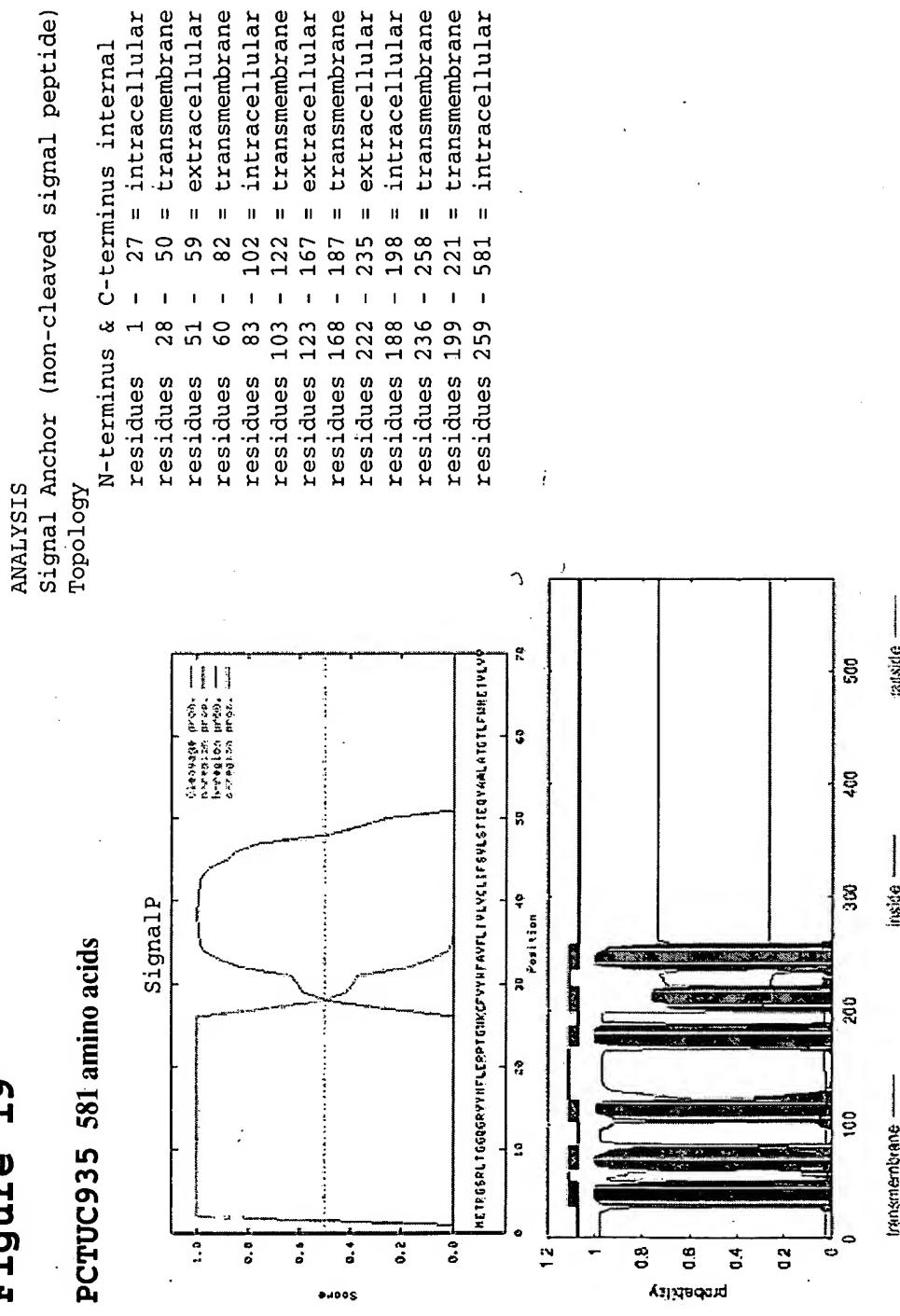


Figure 19



RESULTS
 signal peptide probability = 0.02%
 signal anchor probability = 99.8%
 number of probable transmembrane regions = 6

TMHMM

Figure 20

PCTUC936 806 amino acids

RESULTS
signal peptide probability > 99.9%
maximum cleavage site probability = 75.4%
number of probable transmembrane regions = 2
EXPERIMENTAL EVIDENCE SUPPORTS ONLY TM#1 REGION

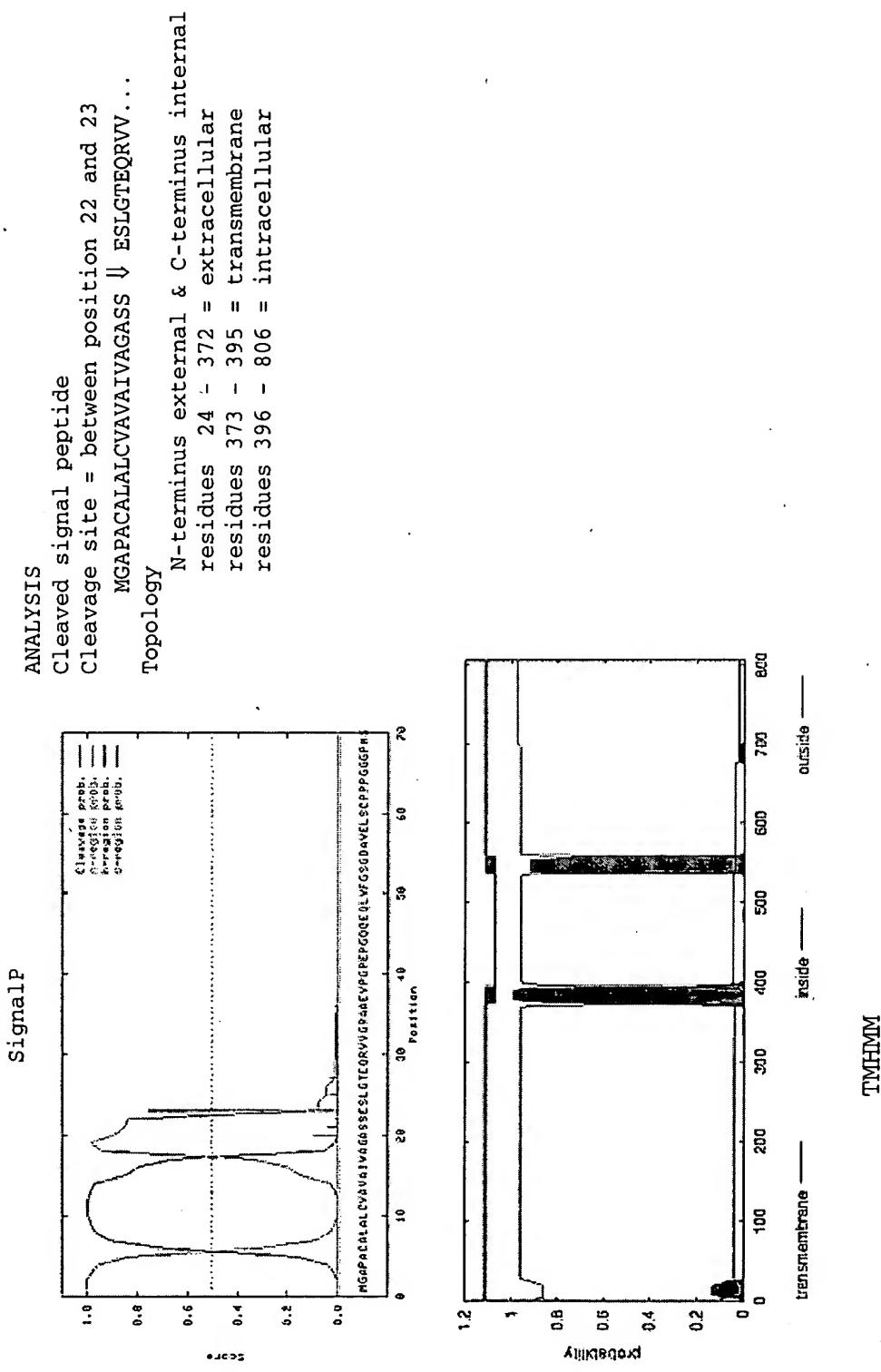


Figure 21

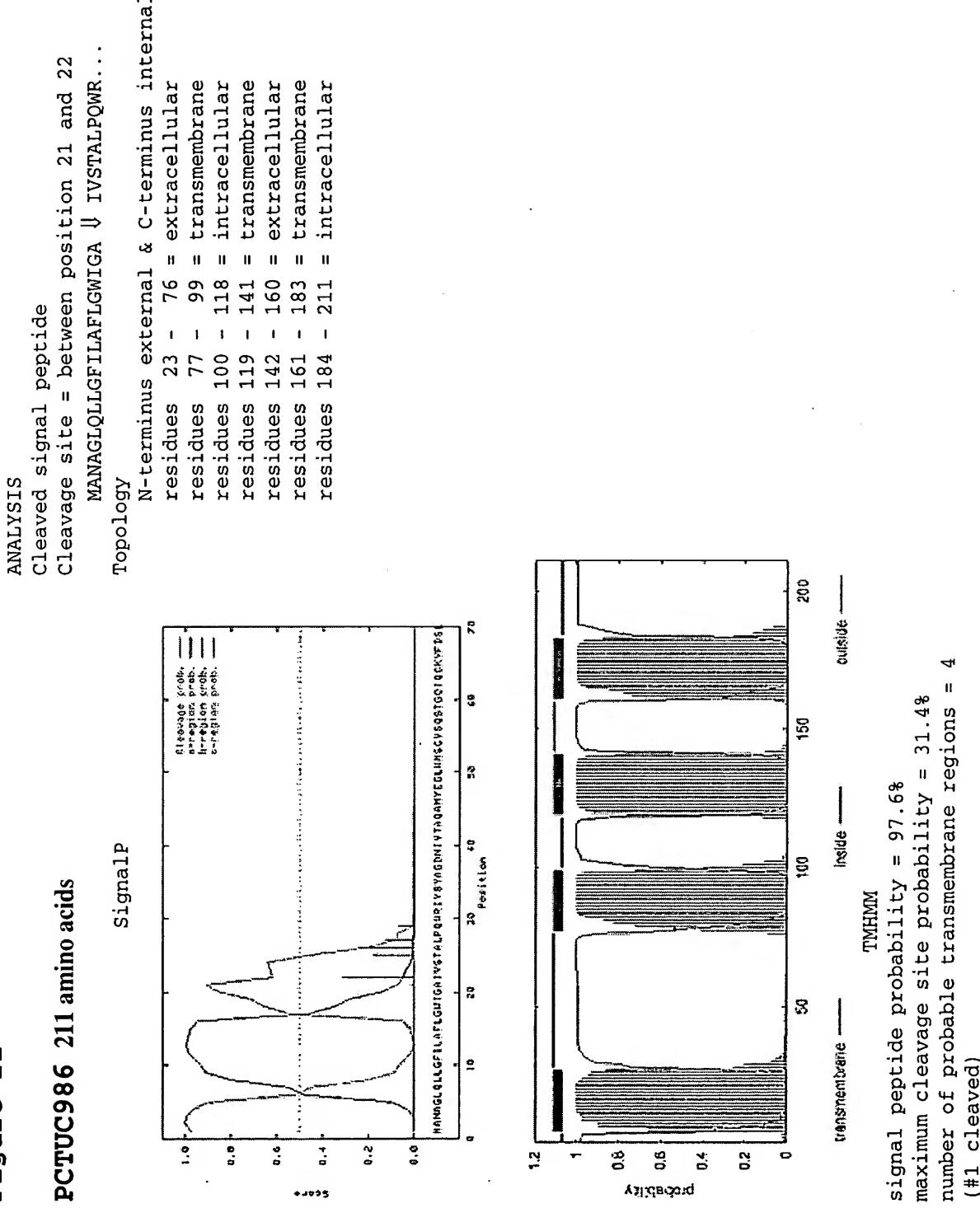
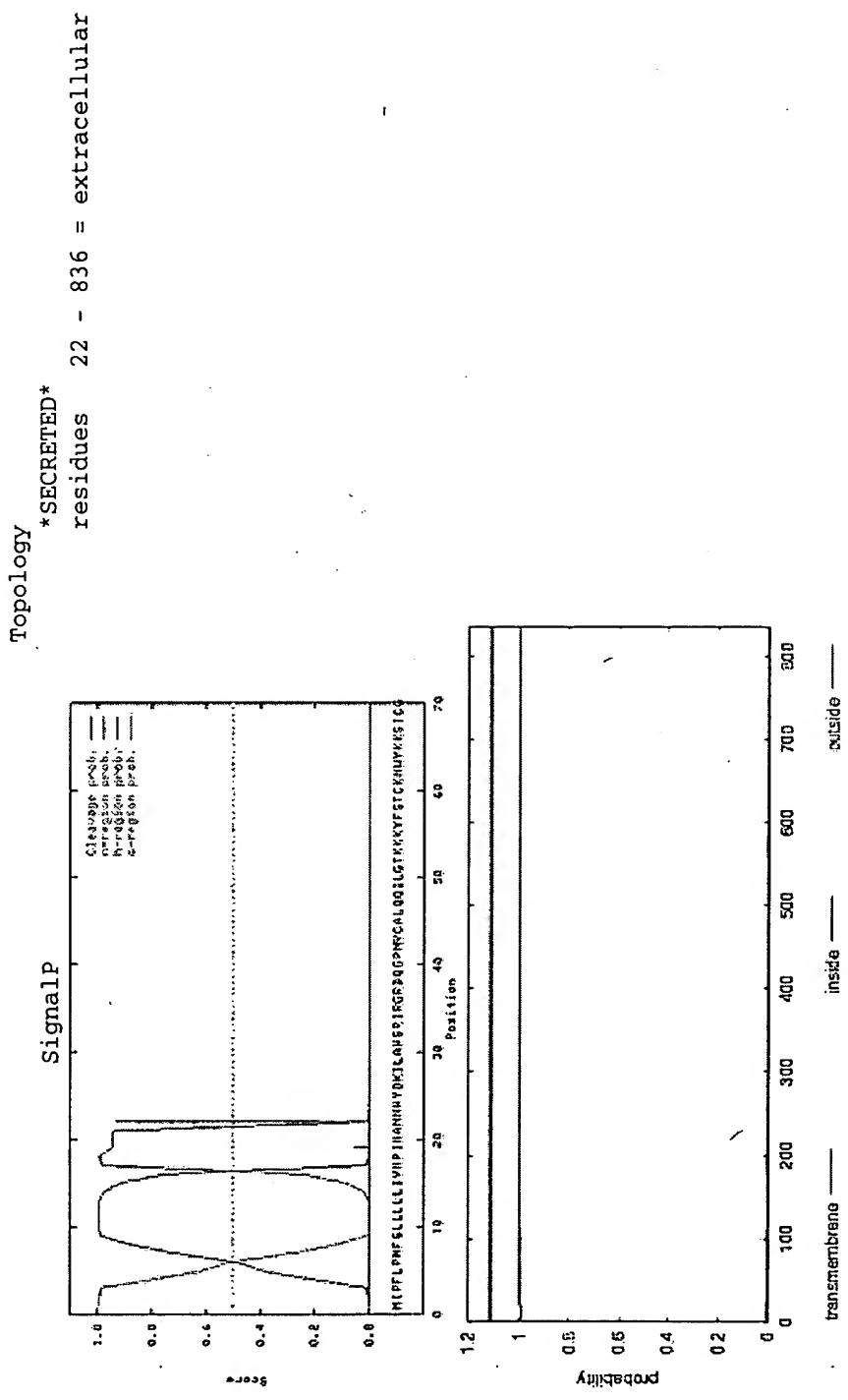


Figure 22

ANALYSIS
Cleaved signal peptide
Cleavage site = between position 21 and 22
MIPFLPMFSSL₂₁LIVNPINA ↓ MNHYDKILAH...

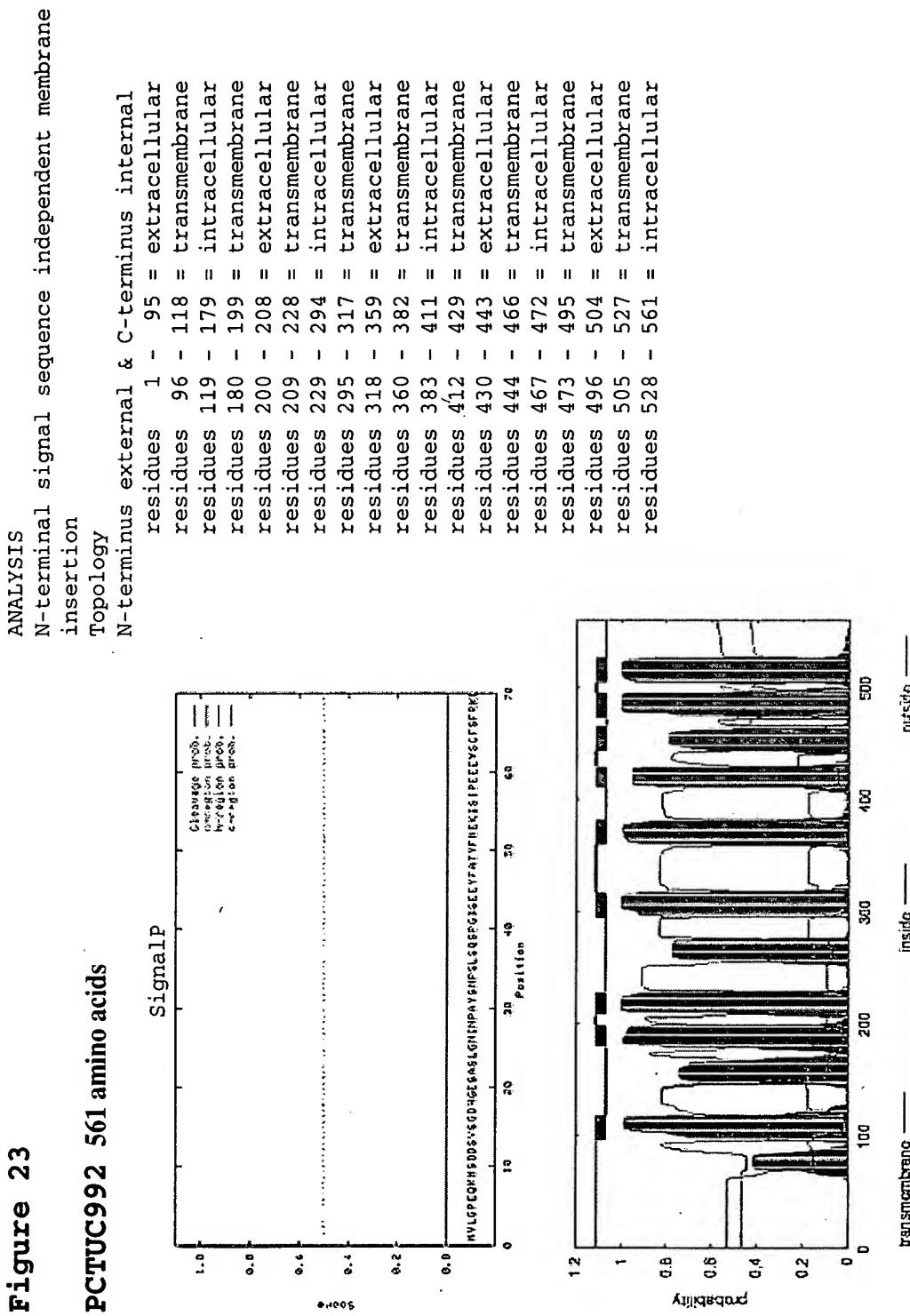


RESULTS
signal peptide probability = 99.9%
maximum cleavage site probability = 93.4%
number of probable transmembrane regions = 0

Figure 23

ANALYSIS

PCTUC992 561 amino acids



RESULTS signal peptide probability = 0%
signal anchor probability = 0%
number of probable transmembrane regions = 9

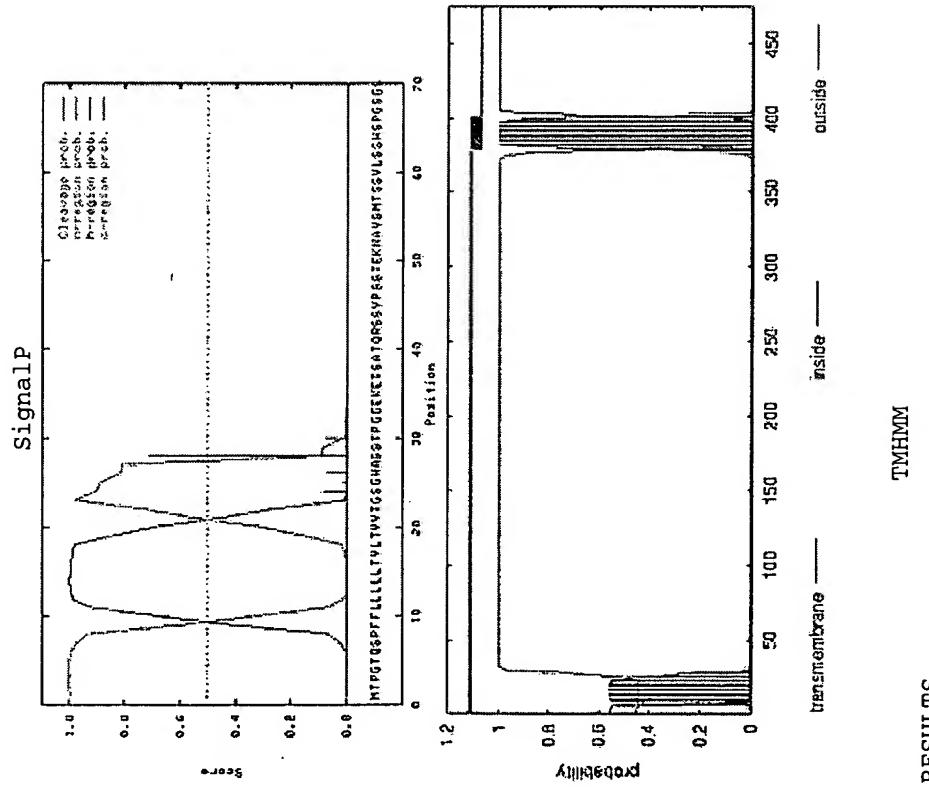
Figure 24

PCTUC1054 475 amino acids

ANALYSIS
Cleaved signal peptide
Cleavage site = between position 27 and 28
MTPGTQSPFFLL.LLTVTGSHA \Downarrow **SSTPGGEKET...**

Topology

N-terminus external & C-terminus internal
residues 28 - 378 = extracellular
residues 379 - 401 = transmembrane
residues 402 - 475 = intracellular



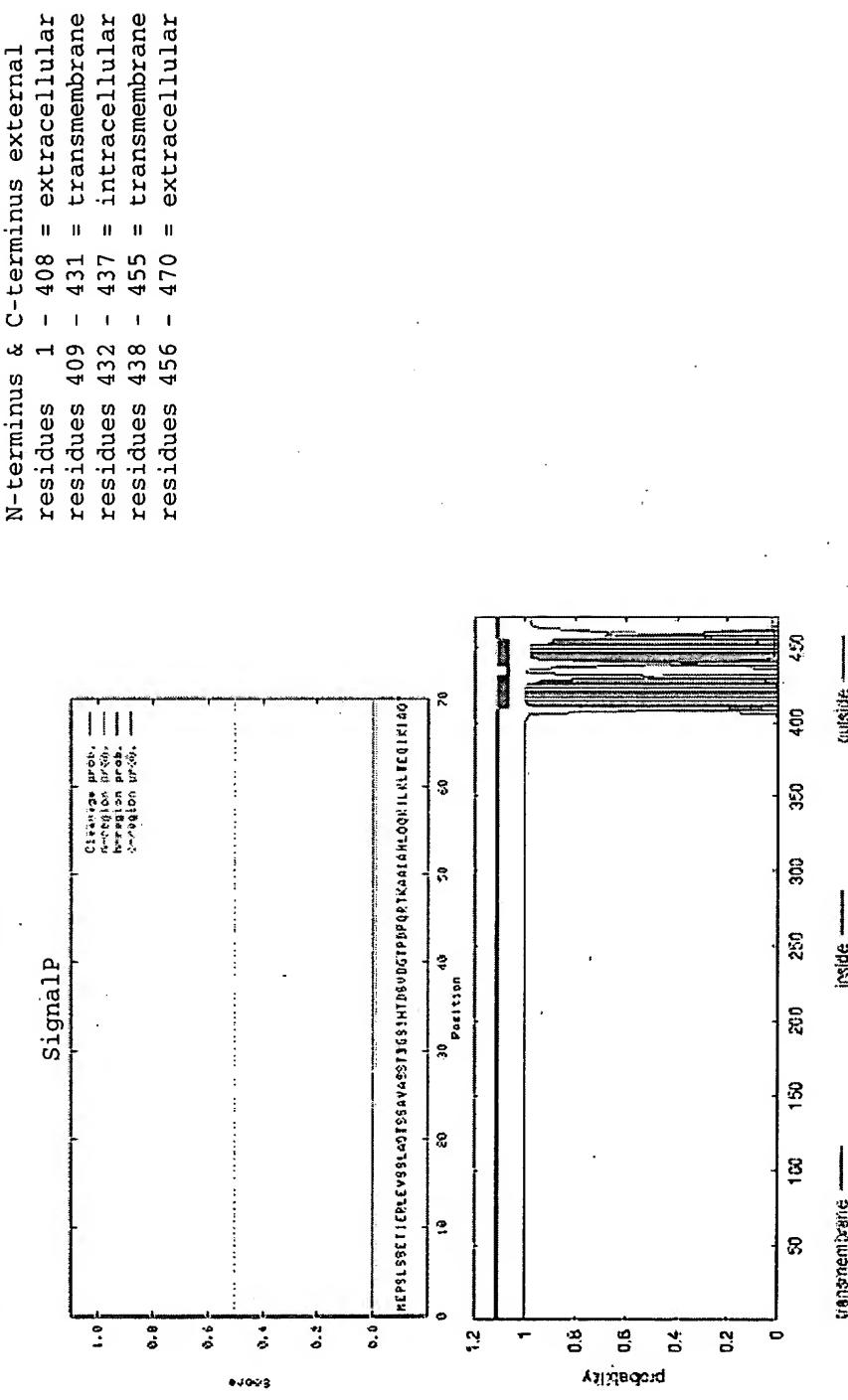
RESULTS
signal peptide probability = 99.8%
maximum cleavage site probability = 71.4%
number of probable transmembrane regions = 1

TMHMM

Figure 25

ANALYSIS
N-terminal signal sequence independent membrane
insertion

PCTUC1061 470 amino acids



RESULTS
signal peptide probability = 0.6%
signal anchor probability = 0.1%
number of probable transmembrane regions = 2

Figure 26

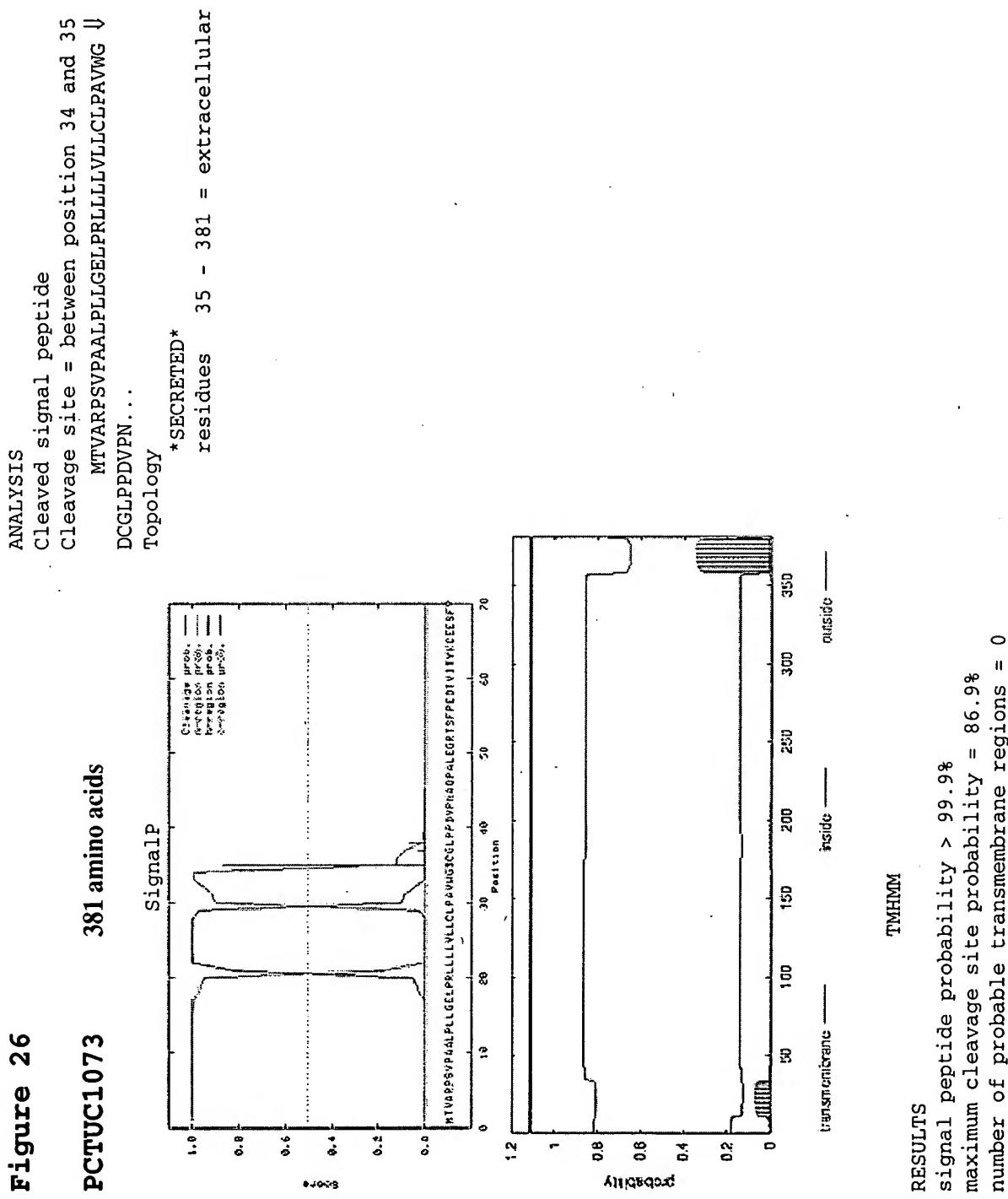
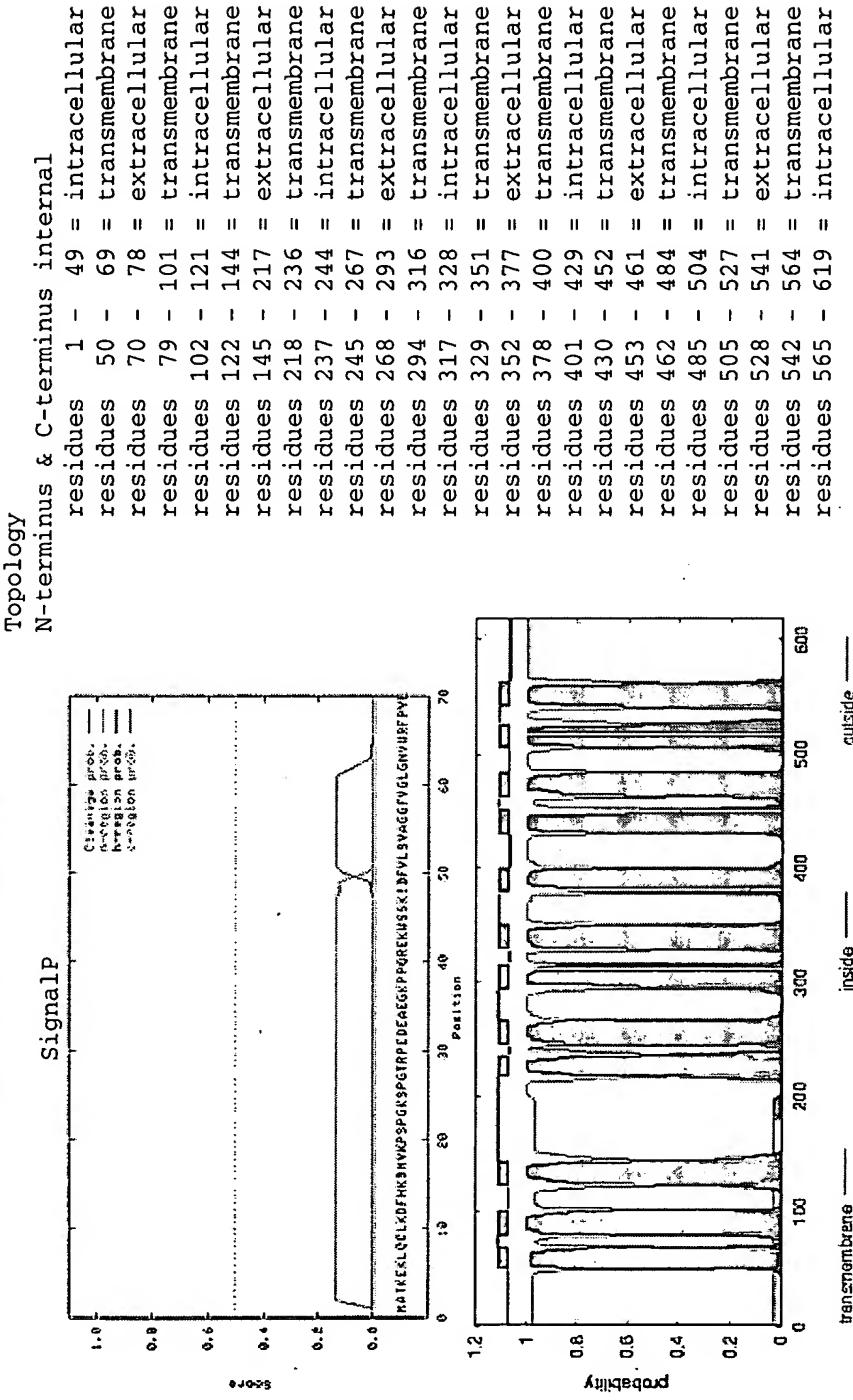


Figure 27

PCTUC1075 619 amino acids

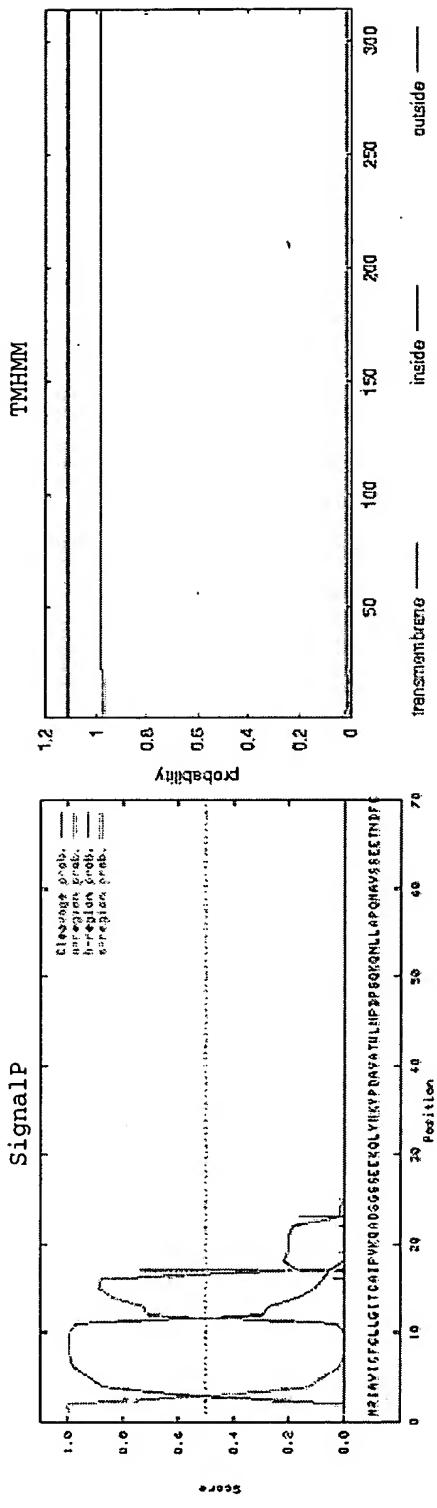
ANALYSIS
N-terminal signal sequence independent membrane
insertion



RESULTS
 signal peptide probability = 0%
 signal anchor probability = 13.9%
 number of probable transmembrane regions = 12

Figure 28

PCTUC1078
314 amino acids



RESULTS

signal peptide probability = 99.9%
maximum cleavage site probability = 73.6%
number of probable transmembrane regions = 0

ANALYSIS

Cleaved signal peptide

Cleavage site = between position 16 and 17

M R I A V I C F C L L G I T C A ↓ I P V K Q A D S G S . . .

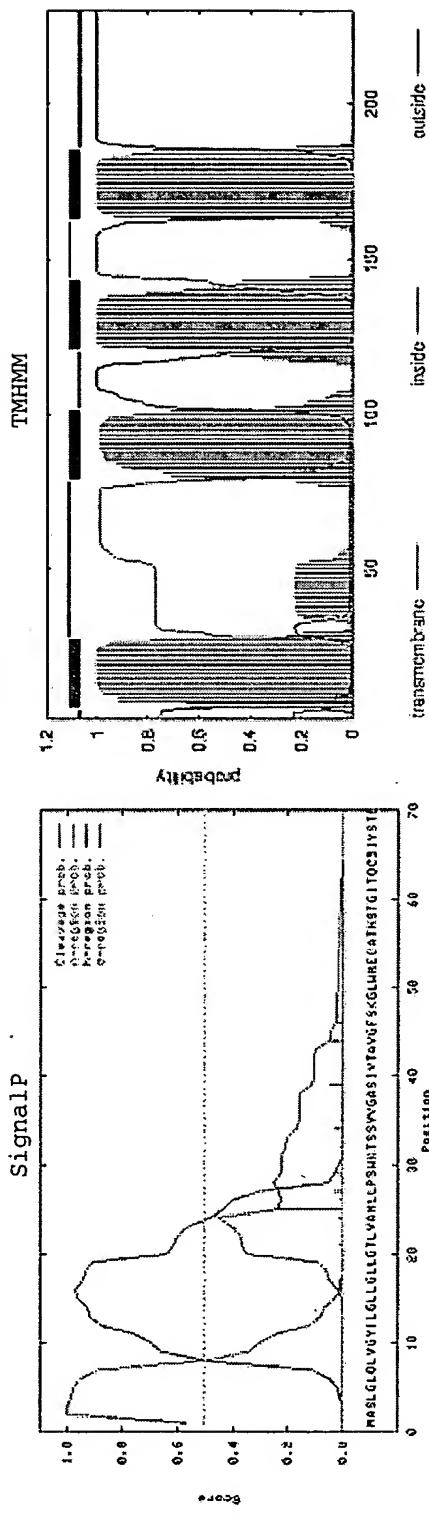
Topology

SECRETED

residues 18 - 314 = extracellular

Figure 29

PCTUUC1082
230 amino acids



signal peptide probability = 57.0%
maximum cleavage site probability = 23.7%
number of probable transmembrane regions = 4 (#1 cleaved)

ANALYSIS

Cleaved signal peptide

Cleavage site = between position 24 and 25

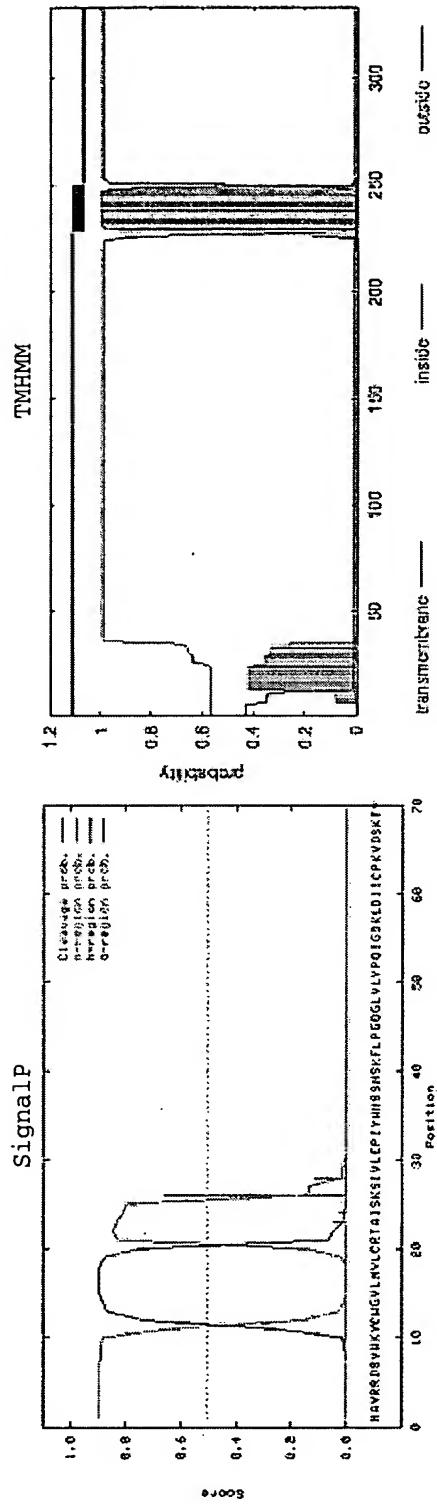
MASLGLQLVGYILQLGILVVA ↓ MLLPSWKTSS ...

Topology

N-terminus external & C-terminus internal
residues 25 - 78 = extracellular
residues 79 - 101 = transmembrane
residues 102 - 120 = intracellular
residues 121 - 143 = transmembrane
residues 144 - 162 = extracellular
residues 163 - 185 = transmembrane
residues 186 - 230 = intracellular

Figure 30

PCTUC1122
333 amino acids



RESULTS

signal peptide probability = 89.5%
maximum cleavage site probability = 65.9%
number of probable transmembrane regions = 1

ANALYSIS

Cleaved signal peptide
Cleavage site = between position 25 and 26

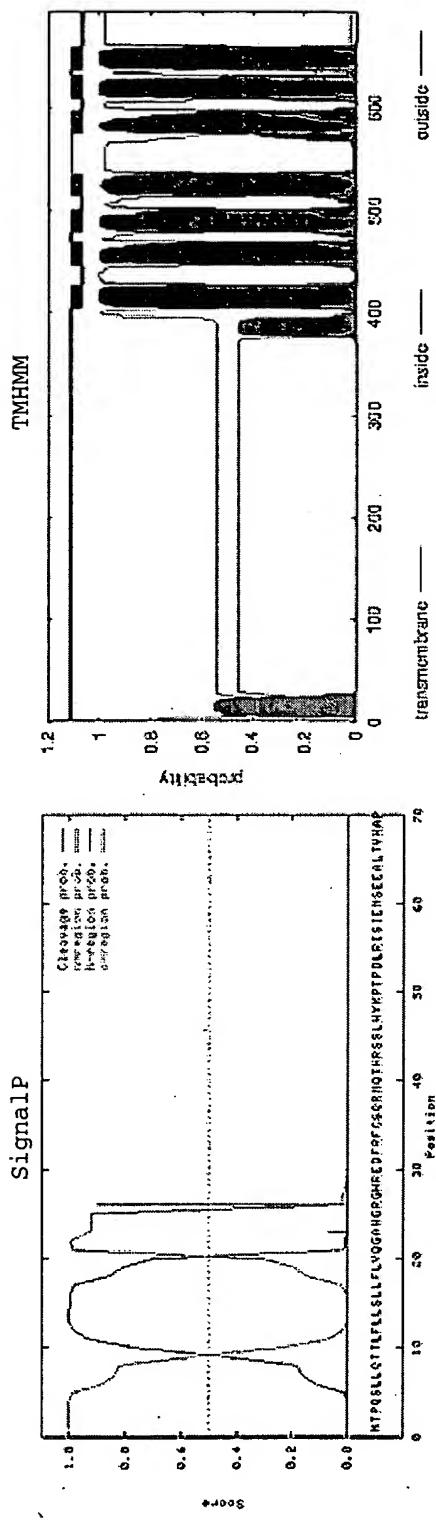
MAVRDRDSWVKYCWGVLMVLCRTAIS ↓ KSIIVLEPIYW...

Topology

N-terminus external & C-terminus internal
residues 26 - 227 = extracellular
residues 228 - 250 = transmembrane
residues 251 - 333 = intracellular

Figure 31

PCTUC250 **693 amino acids**



RESULTS

signal peptide probability > 99.9%
maximum cleavage site probability = 90.4%
number of probable transmembrane regions = 7

ANALYSIS

Cleaved signal peptide

Cleavage site = between position 25 and 26

MTPQSLLQTRFLFLSLLFLVQGAHG ↓ RGHREDFRFC

Topology

residues 502 - 513	= intracellular
residues 514 - 536	= transmembrane
residues 537 - 574	= extracellular
residues 575 - 597	= transmembrane
residues 598 - 608	= intracellular
residues 609 - 631	= transmembrane
residues 632 - 636	= extracellular
residues 637 - 659	= transmembrane
residues 660 - 693	= intracellular